

FORM PTO-1390  
(REV. 11-94)

U.S. DEPARTMENT OF COMMERCE  
PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

6750-018

**TRANSMITTAL LETTER TO THE UNITED STATES  
DESIGNATED/ELECTED OFFICE (DO/EO/US)**

**09/831631**

INTERNATIONAL APPLICATION NO.  
PCT/US99/26671

INTERNATIONAL FILING DATE  
November 12, 1999

PRIORITY DATE CLAIMED  
November 13, 1998

**TITLE OF INVENTION**

CONTRACEPTIVE ANTIBODY VACCINES

**APPLICANT(S) FOR DO/EO/US**

Ronald Martin BURCH and David Alex SACKLER

Applicant herewith submits to the United States Designated/ Elected Office (DO/EO/US) the following items under 35 U.S.C. 371:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This is an express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
  - a. ☒ is transmitted herewith (required only if not transmitted by the international Bureau).
  - b. ☐ has been transmitted by the International Bureau.
  - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US)
6. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
  - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
  - b. ☐ have been transmitted by the International Bureaus.
  - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
  - d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 37(c)(3)).
9. ☒ An unexecuted oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

**Items 11. to 16. below concern document(s) or information included:**

11. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. ☒ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. ☒ A **FIRST** preliminary amendment.  
☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information:
  1. Copy of Preliminary Search Report
  2. Copy of WO 00/29443

INTERNATIONAL APPLICATION NO.  
PCT/US99/26671

09/831631

INTERNATIONAL FILING DATE  
November 12, 1999

JC18 Rec'd PCT/PTO 1 0 MAY 2001

17. ☒ The U.S. National Fee (35 U.S.C. 371(c)(1)) and other fees as follows:

CLAIMS				
(1)FOR	(2)NUMBER FILED	(3)NUMBER EXTRA	(4)RATE	(5)CALCULATIONS
TOTAL CLAIMS	37 - 20	17	X \$ 18.00	\$ 306.00
INDEPENDENT CLAIMS	3 - 3	0	X \$ 80.00	0.00
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$ 270.00	\$ 270.00
BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5)): <b>CHECK ONE BOX ONLY</b>				
<input type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482)			\$ 690	
<input type="checkbox"/> No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2))			\$ 710	
<input type="checkbox"/> Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO			\$ 1000	
<input checked="" type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2) to (4)			\$ 100	\$ 100.00
<input type="checkbox"/> Filing with EPO or JPO search report			\$ 860	
Surcharge of \$130.00 for furnishing the National fee or oath or declaration later than 20 <input checked="" type="checkbox"/> 30 mos. from the earliest claimed priority date (37 CFR 1.492(e)).				\$ 130.00
TOTAL OF ABOVE CALCULATIONS				= 806.00
Reduction by 1/2 for filing by small entity, if applicable. Affidavit must be filed also. (Note 37 CFR 1.9, 1.27, 1.28).				- \$ 0.00
SUBTOTAL				= 806.00
Processing fee of \$130.00 for furnishing the English Translation later than 30 mos. from the earliest claimed priority date (37 CFR 1.492(f)).				+ 0
TOTAL FEES ENCLOSED				\$ 806.00

- a. ☐ A check in the amount of \$ to cover the above fees is enclosed.
- b. ☒ Please charge Deposit Account No. 16-1150 in the amount of \$806.00 to cover the above fees. A copy of this sheet is enclosed.
- c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 16-1150. A copy of this sheet is enclosed.

18. ☐ Other instructions  
n/a

19. ☒ All correspondence for this application should be mailed to  
PENNIE & EDMONDS LLP  
1155 AVENUE OF THE AMERICAS  
NEW YORK, NEW YORK 10036-2711

20. ☒ All telephone inquiries should be made to (212) 790-2803

Adriane M. Antler  
NAME

SIGNATURE

REGISTRATION NUMBER

May 10, 2001  
DATE

by Margaret B. Bonifant  
Reg No. 40,922

09/1831631  
JC18 Rec'd PCT/PTO 10 MAY 2001

Express Mail No.: EL 501 638 835 US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Ronald Martin Burch and David Alex Sackler

Application No.: To Be Assigned; National      Group Art Unit: To Be Assigned  
Stage Application of International  
Application No. PCT/US99/26671, filed  
November 12, 1999

Filed: Concurrently Herewith      Examiner: To Be Assigned

For: CONTRACEPTIVE ANTIBODY      Attorney Docket No.: 6750-018  
VACCINES

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

Prior to examination of the above-identified application, please enter the following amendment and consider the remarks made below.

IN THE SPECIFICATION:

Please amend the specification as follows:

On page 1, after the title and before the heading "1. FIELD OF THE INVENTION," please insert the following paragraph:

-- This is a national stage application of International Application PCT/US99/26671, filed November 12, 1999, which was published under PCT Article 21(2) as PCT Publication No. WO 00/29443 in English, and which claims the benefit of United States Provisional Application Serial No. 60/108,325, filed November 13, 1998. Both International Application PCT/US99/26671 and United States Provisional Application Serial No. 60/108,325 are hereby incorporated by referenced in their entireties. --

**REMARKS**

Applicants have amended the specification to include reference to International Application PCT/US99/26671, of which the present application is national stage application, and United States Provisional Application Serial No. 60/108,325. Also, pursuant to 37 C.F.R. § 1.78(a)(2), the first sentence of the specification indicates that International Application PCT/US99/26671 was published under PCT Article 21(2) in English. Accordingly, these amendments to the specification do not introduce new matter.

Applicants respectfully request that these amendments and remarks be entered and made of record in the present application.

Respectfully submitted,

Date May 10, 2001

Adriane M. Antler 32,605  
Adriane M. Antler (Reg. No.)

Margaret B. Brivanlou 40,922  
By: Margaret B. Brivanlou (Reg. No.)

PENNIE & EDMONDS LLP  
1155 Avenue of the Americas  
New York, New York 10036-2711  
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09831631 092103  
101 Rec'd PCT/PTO 21 SEP 2001  
09/831631  
Express Mail No.: EL 501 641 619 US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Burch *et al.*

Application No.: 09/831,631

Group Art Unit: To Be Assigned

Filed: National Stage of PCT Application  
PCT/US99/26671 filed November 12,  
1999

Examiner: To Be Assigned

Attorney Docket No.: 6750-018

For: CONTRACEPTIVE ANTIBODY  
VACCINES

New York, NY  
September 21, 2001

**PRELIMINARY AMENDMENT UNDER 37 C.F.R. § 1.115**

Commissioner for Patents  
Washington, D.C. 20231

Sir:

Prior to examining the above-identified application on the merits, please enter the following amendments and consider the remarks below. Accompanying this Preliminary Amendment is Exhibit A, a marked up version of the replacement paragraphs of the specification.

**IN THE SPECIFICATION:**

Please amend the specification as follows:

On page 6, at line 22, please amend the paragraph beginning "Figures 7A and B." as follows:

--Figures 7A and B. (A) The amino acid sequence (SEQ ID NO. 30) and corresponding nucleotide sequence (SEQ ID NO. 29) for the consensus light chain variable region ConVL1. (B) The amino acid sequence (SEQ ID NO. 32) and corresponding nucleotide sequence (SEQ ID NO. 31) for the consensus heavy chain variable region ConVH1.--

On page 7, at line 11, please amend the paragraph beginning “Figure 11.” as follows:

--Figure 11. Nucleotide sequences of the oligonucleotides (DSABL-1 (SEQ IS NO: 33), DSABL-1c (SEQ IS NO: 34), MSAL-CDR1-1 (SEQ IS NO: 35), MSAL-CDR1-1c (SEQ IS NO: 36), HMVL1 (SEQ IS NO: 37), HMVL2 (SEQ IS NO: 38), HMVL3 (SEQ IS NO: 39), HMVL5 (SEQ IS NO: 40), HMVL8 (SEQ IS NO: 41), HMVL9 (SEQ IS NO: 42), HMVL10 (SEQ IS NO: 43), HMVL6 (SEQ IS NO: 44), HMVL4 (SEQ IS NO: 45), and HMVL7 (SEQ IS NO: 46)) used to construct the MSA1 and MSALVAC-1 variable regions.--

On page 7, at line 13, please amend the paragraph beginning “Figures 12A-C.” as follows:

--Figures 12A-C. (A) Nucleotide sequence for the MSA-63 epitope (SEQ ID NO: 19). (B) Amino acid sequence of the MSA-63 epitope encoded by the nucleotide sequence of Figure 12A (SEQ ID NO: 20). (C) MSA-63 oligonucleotides used to construct a modified variable region. Each oligo overlaps for five codons and transitions the entire sequence of Figure 12A (MSA1 (SEQ ID NO: 21), MSA2 (SEQ ID NO: 22), MSA3 (SEQ ID NO: 23), MSA4 (SEQ ID NO: 24), MSA5 (SEQ ID NO: 25), MSA6 (SEQ ID NO: 26), MSA7 (SEQ ID NO: 27)).--

On page 7, at line 17, please amend the paragraph beginning “Figures 13A-C.” as follows:

--Figures 13 A-C. (A) Nucleotide sequence for the SP-10 epitope (SEQ ID NO: 9). (B) Amino acid sequence of the SP-10 epitope encoded by the nucleotide sequence of Figure 13A (SEQ ID NO: 10). (C) Oligonucleotides of Sp-10 used to construct a modified variable region (SP1 (SEQ ID NO:11), SP2 (SEQ ID NO:12), SP3 (SEQ ID NO:13), SP4 (SEQ ID NO:15), SP5 (SEQ ID NO:17), and SP6 (SEQ ID NO:18)). SP3a (SEQ ID NO:14) and SP4a (SEQ ID NO:16) are modified to change the codons encoding certain cysteine residues to codons encoding alanine residues.--

On page 7, at line 22, please amend the paragraph beginning “Figure 14.” as follows:

--Figure 14. Oligonucleotides of LDH-C4 epitope sequence for construction of a modified variable region gene containing a LDH-C<sub>4</sub> (LDH1 (SEQ ID NO: 47), and LDH2 (SEQ ID NO: 48)).--

On page 7, at line 24, please amend the paragraph beginning “Figure 15.” as follows:

--Figure 15. Nucleotide (SEQ ID NO: 71) and amino acid (SEQ ID NO: 72) sequences of the consensus contraceptive light chain variable region. --

On page 7, at line 26, please amend the paragraph beginning “Figure 16 A-B.” as follows:

--Figures 16 A-B. (A) Sequences of oligos used in the construction of 2CAVHCOL1 (VHC1 (SEQ ID NO: 49), VHC2 (SEQ ID NO: 50), VHC3 (SEQ ID NO: 51), VHC4 (SEQ ID NO: 52), VHC5 (SEQ ID NO: 53), VHC6 (SEQ ID NO: 54), VHC7 (SEQ ID NO: 55), VHC8 (SEQ ID NO: 56), VHC9 (SEQ ID NO: 57), and VHC10 (SEQ ID NO: 58)). (B) Sequences of oligos used in the construction of 2CAVLCOL1 (VLC1 (SEQ ID NO: 59), VLC2 (SEQ ID NO: 60), VLC3 (SEQ ID NO: 61), VLC4 (SEQ ID NO: 62), VLC5 (SEQ ID NO: 63), VLC6 (SEQ ID NO: 64), VLC7 (SEQ ID NO: 65), VLC8 (SEQ ID NO: 66), VLC9 (SEQ ID NO: 67), VLC10 (SEQ ID NO: 68), VLC11 (SEQ ID NO: 69), and VLC12 (SEQ ID NO: 70)).--

On page 38, at line 3, please amend the paragraph beginning “In order to confirm” as follows:

--In order to confirm correct gene sequences of the engineered variable region genes and to eliminate the possibility of unwanted mutations generated during the construction procedure, DNA sequencing was performed using M13/pUC reverse primer (5'AACAGCTATGACCATG 3' (SEQ ID NO:1)) for the clones as well as PCR gene products using 5' end 20 base primer ( 5' GAATT CATGGCTTG

GGTGTG 3' (SEQ ID NO: 2)) on automated ABI 377 DNA Sequencer. All clones were confirmed to contain correct sequences.--

On page 40, at line 23, please amend the table beginning "Table 6." as follows:

**Table 6.      Biotin-Labeled Peptides Derived from CDR Sequences of Mab 31.1**

**Peptide ID    Sequence**

COL311 L1	biotin-N-Thr-Ala-Lys-Ala-Ser-Gln-Ser-Val-Ser-Asn-Asp-Val-Ala (SEQ ID NO: 3)
COL311 L2	biotin-N-Ile-Tyr-Tyr-Ala-Ser-Asn-Arg-Tyr-Thr (SEQ ID NO: 4)
COL311 L3	biotin-N-Phe-Ala-Gln-Gln-Asp-Tyr-Ser-Ser-Pro-Leu-Thr (SEQ ID NO: 5)
COL311 H1	biotin-N-Phe-Thr-Asn-Tyr-Gly-Met-Asn (SEQ ID NO: 6)
COL311 H2	biotin-N-Ala-Gly-Trp-Ile-Asn-Thr-Tyr-Thr-Gly-Glu-Pro-Thr-Tyr-Ala- Asp-Asp-Phe-Lys-Gly (SEQ ID NO: 7)
COL311 H3	biotin-N-Ala-Arg-Ala-Tyr-Tyr-Gly-Lys-Tyr-Phe-Asp-Tyr (SEQ ID NO: 8)

On page 41, at line 25, please amend the paragraph beginning "The nucleotide and protein sequences" as follows:

--The nucleotide and protein sequences of the SP-10 epitope are:

GAA TTC CAG CCT TCA GGT GAA CAT GGC TCC GGT GAA CAG CCT TCT  
GGT GAG CAG GCC TCG GGT GAA CAG CCT TCA GGT GAG CAC GCT TCA  
GGG GAA CAG GCT TCA GGT GCA CCA ATT TCA AGC ACA TCT ACA GGC  
ACA ATA TTA AAT TGC TAC ACA TGT GCT TAT ATG AAT GAT CAA GGA  
AAA TGT CTT CGT GGA GAG GGA ACC TGC ATC ACT CAG AAT TC (SEQ  
ID NO: 9);

Gln Pro Ser Gly Glu His Gly Glu Gln Pro Ser Gly Glu Gln Ala Ser Gly Glu Gln Pro  
Ser gly Glu His Ala Ser Gly Glu Gln Ala Ser Gly Ala Gln Ile Ser Ser Thr Ser Thr Gly

Thr Ile Leu Asn Cys Tyr Thr Cys Ala Tyr Met Asn Asp Gln Gly Lys Cys Leu Arg Gly  
Glu Gly Thr Cys Ile Thr Gln Asn (SEQ ID NO: 10).--

Beginning on page 41, at line 33, continuing to page 42, line 20, please amend the paragraph beginning "The replacement of an antibody's CDR" as follows:

--The replacement of an antibody's CDR with another epitope is made easier by the fact that the variable region sequence of antibodies are relatively short, and are known. One is then able to synthetically generate a series of complementary oligonucleotides that, when annealed and ligated, reconstruct the entire coding region of variable region portion of the gene. In this manner, the CDR is replaced with sequences of the epitope of interest, in this example, SP-10. The following is a list of the sequences of the oligonucleotides designed for cloning SP-10 epitopes into the CDR:

**Oligo SP 1 (SEQ ID NO: 11):**

GAA TTC CAG CCT TCA GGT GAA CAT GGC TCC GGT GAA CAG CCT TCT  
GGT GAG CAG GCC TCG GGT GAA CAG CCT TAG,

**Oligo SP 2 (SEQ ID NO: 12):**

GTG AGC ACG CTT CAG GGG AAC AGC CTT CAG GTG CAC CAA TTT CAA  
GCA CAT CTA CAG GCA CAA TAT TAA ATT GCT,

**Oligo SP 3 (SEQ ID NO: 13):**

ACA CAT GTG CTT ATA TGA ATG ATC AAG GAA AAT GTC TTC GTG GAG  
AGG GAA CCT GCA TCA CTC AGA ATT C,

**Oligo SP 3a(3Cys-> Ala) (SEQ ID NO: 14):**

ACA CAG CAG CTT ATA TGA ATG ATC AAG GAA AAG CAC TTC GTG GAG  
AGG GAA CCG CAA TCA CTC AGA ATT C,

**Oligo SP 4 (SEQ ID NO: 15):**

GAA TTC TGA GTG ATG CAG GTT CCC TCT CCA CGA AGA CAT TTT CCT  
TGA TCA TTC ATA TAA GCA CAT GTG TAG CAA TTT A,

**Oligo SP 4a (3Cys->Ala) (SEQ ID NO: 16):**

GAA TTC TGA GTG ATT GCG GTT CCC TCT CCA CGA AGT GCT TTT TGA  
TGA TCA TTC ATA TAA GCT GCT GTG TAG CAA TTT A,

**Oligo SP 5 (SEQ ID NO: 17):**

ATA TTG TGC CTG TAG ATG TGC TTG AAA TTG GTG CAC CTG AAG CCT  
GTT CCC CTG AAG CGT GCT CAC CTG AAG GCT,

**Oligo SP 6 (SEQ ID NO: 18):**

GTT CTC CCG AGG CCT GCT CAC CAG AAG GCT GTT CAC CGG AGC CAT  
GTT CAC CTG AAG GCT GGA ATT C.--

Beginning on page 42, at line 25, continuing to page 43, line 17, please amend the paragraph beginning "Practically, the first two amino acid codons" as follows:

--Practically, the first two amino acid codons of the sperm cell specific epitope, MSA-63, an oligonucleotide encoding residues 143 and 144 (i.e. GTC GGC, *infra*), is cloned into the immunoglobulin CDR, using the methods described *infra*.

The MSA-63 DNA sequence encoding the epitope:

GTC GGC AGC CTC CGA AGC AGC CCG CTC CAG AGC CCG CTG CTC CGA  
CCG CTC GTC CAG AGC AGC CTC TGC TTG CTG TTC CTC TTG CTG CGA  
TAC AGC TGC GGC GAC GGC AGC TGC AGC CGA CGA TAC TGC GAC TTG  
ACG GTG TGC CGG CGA ATG TAC TTG CTG CTG CGA TTC ACG GAC CCG  
CCG CTC CCG CAG ACG TGC TGC GTC TTG AGC (SEQ ID NO: 19)

The MSA-63 protein sequence epitope encoded by the nucleic acid sequence above, which starts at amino acid 143 and ends at 233.

Gln Pro Ser Glu Ala Ser Ser Gly Glu Val Ser Gly Asp Glu Ala Gly Glu Gln Val Ser  
Ser Glu Thr Asn Asp Lys Glu Asn Asp Ala Met Ser Thr Pro Leu Pro Ser Thr Ser Ala  
Ala Ile Thr Leu Asn Cys His Thr Cys Ala Tyr Met Asn Asp Asp Ala Lys Cys Leu Arg  
Gly Glu Gly Val Cys Thr Thr Gln Asn Ser (SEQ ID NO: 20)

For the second two amino acid codons, an oligonucleotide encoding residues 144 and 145 is utilized (*i.e.*, GGC AGC). For the third, 145 and 146 and so on until the entire epitope is synthesized and inserted into the CDR, two amino acids at a time. For peptides three amino acids in length, an oligonucleotide encoding residues 143 to 146

is synthesized. The second oligonucleotide synthesized encodes residues 146 to 148. The third encodes residues 148 to 150, and this continues until the entire epitope is covered in this fashion. The next oligonucleotide that is synthesized is four amino acid codons in length. It begins with residues 143 to 146, its second segment is equivalent to residues 145 to 148, its third segment corresponds to residues 147 to 150, and so on until the entire epitope is transitioned in this fashion. The next oligonucleotide synthesized contains five amino acid codons with two overlapping with the previous. For example, the first oligonucleotide encodes residues 143 to 147, and the second residues 146 to 150. This pattern continues until the entire epitope has been transitioned. The next construct encoding an epitope uses nucleotides for six amino acid codons with two overlapping with the previous codons as described *infra*.--

On page 43, at line 24, please amend the paragraph beginning “In a specific example,” as follows:

--In a specific example, oligomers have been designed which scan the entire length of the MSA-63 epitope and encode 15 amino acids. Each oligo overlaps with the previous one for the equivalent of five amino acids. MSA-63 oligos encoding 15 amino acids, with overlap of five amino acids each:

**MSA1:** GTC GGC AGC CTC CGA AGC AGC CCG CTC CAG AGC CCG CTG  
CTC CGA (SEQ ID NO: 21)

**MSA2:** AGC CCG CTG CTC CGA CCG CTC GTC CAG AGC AGC CTC TGC  
TTG CTG (SEQ ID NO: 22)

**MSA3:** AGC CTC TGC TTG CTG TTC CTC TTG CTG CGA TAC AGC TGC  
GGC GAC (SEQ ID NO: 23)

**MSA4:** TAC AGC TGC GGC GAC GGC AGC TGC AGC CGA CGA TAC TGC  
GAC TTG (SEQ ID NO: 24)

**MSA5:** CGA TAC TGC GAC TTG ACG GTG TGC ACG CGA ATG TAC TTG  
CTG CTG (SEQ ID NO: 25)

**MSA6:** ATG TAC TTG CTG CTG CGA TTC ACG GAC GCG CCG CTC CCG  
CAG ACG (SEQ ID NO: 26)

**MSA7:** CGA TTC ACG GAC GCG CCG CTC CCG CAG ACG TGC TGC GTC  
TTG AGC (SEQ ID NO: 27)--

On page 44, at line 1, please amend the paragraph beginning "Antibodies in which a portion" as follows:

--Antibodies in which a portion of the MSA-63 antigen has been inserted into CDR1, *i.e.*, where residues Lys24 through Ala34 of the consensus contraceptive light chain, the sequence of which is in Figure 15, are replaced with the sequence Gln-Pro-Ser-Glu-Ala-Ser-Ser-Gly-Glu-Val-Ser-Gly-Asp-Glu-Ala-Gly-Glu (SEQ ID NO: 28). The antibody, MSA1, can be constructed using the oligonucleotides provided in Figure 11 in the scheme provided in Figure 8 and described below, where the identities of oligonucleotides 1-12 are indicated in Table 7. The antibody MSA1VAC can also be constructed using the oligos of Figure 11 by the scheme of Figure 8, as indicated in Table 7. MSA1VAC is the same as MSA1 except that the cysteine at position 23 of the light chain variable region has been replaced with alanine. These light chains can be expressed with the heavy chain consensus sequence CONVH1, the sequence of which is provided in Figure 7B, and the construction of which can be accomplished with the oligonucleotides as indicated in Table 4. These single stranded oligonucleotides sequences are annealed to create cohesive double stranded DNA fragments suitable for ligation as diagramed in Figure 8, along with oligonucleotides encoding the remainder of the consensus variable region, to construct the variable region gene. For the MSA-63 containing variable regions MSA1 and MSA1VAC the oligonucleotides corresponding to oligonucleotides 1 to 10, or 1 to 12, of Figure 8 are provided in Table 7, and the sequences of these oligonucleotides are provided in Figure 11. Specifically, oligonucleotides of about 70 bases in length corresponding to the sequences of interest with 20 base overlapping regions are synthesized (GenoSys Biotech Inc.). Each oligonucleotide is 5' phosphorylated as follows: 25µl of each oligo is incubated for one hour in the presence of T<sub>4</sub> polynucleotide kinase and 50 mM ATP in appropriate buffer at 37°C. The enzyme is heat killed and the reaction stopped by heating for ten minutes at 70°C followed by ethanol precipitation with sodium acetate. The oligos are then resuspended in TE buffer (10 mM Tris, pH 8.0, 1 mM EDTA).--

After the Abstract of the Disclosure, please insert the Sequence Listing as independently numbered page 1.

**REMARKS**

Applicants have amended the specification pursuant to 37 C.F.R. § 1.821(d) to identify the sequences disclosed therein by their respective SEQ ID NOs as found in the Sequence Listing being submitted concurrently herewith and to add the Sequence Listing provided herewith to the application. Applicants have also amended the specification to correct a typographical error; a three letter amino acid code has been corrected to 'Gln' from 'Gin' (page 41, line 31), which is an obvious typographical error recognized by the skilled artisan. No new matter is introduced by virtue of these amendments, and the amendments are fully supported by the specification of the subject application and the claims as originally filed. Accordingly, Applicants respectfully request that these amendments and remarks be entered and made of record in the present application.

No fee, other than the extension fee, is believed to be due for the submission of this Amendment. Should any fees be required, however, please charge such fees to Pennie & Edmonds LLP Deposit Account No. 16-1150.

Respectfully submitted,

Dated: September 21, 2001

Adrianne M. Antler 32.605  
Adrianne M. Antler (Reg. No.)

**PENNIE & EDMONDS LLP**  
1155 Avenue of the Americas  
New York, New York 10036-2711  
(212) 790-9090  
Attorneys For Applicants

Attachment:

Exhibit A: Marked up version of the replacement paragraphs of the specification.

By Margaret B. Brisoulas  
Reg No. 40,922

## EXHIBIT A

### Marked up Version of the Replacement Paragraphs of the Specification

**Matter that has been deleted from the paragraphs is indicated by brackets and matter that has been added to the paragraphs is indicated by underlining.**

On page 6, at line 22, please amend the paragraph beginning “Figures 7A and B.” as follows:

Figures 7A and B. (A) The amino acid sequence (SEQ ID NO. 30) and corresponding nucleotide sequence (SEQ ID NO. 29) for the consensus light chain variable region ConVL1. a(B) The amino acid sequence (SEQ ID NO. 32) and corresponding nucleotide sequence (SEQ ID NO. 31) for the consensus heavy chain variable region ConVH1.

On page 7, at line 11, please amend the paragraph beginning “Figure 11.” as follows:

Figure 11. Nucleotide sequences of the oligonucleotides (DSABL-1 (SEQ IS NO: 33), DSABL-1c (SEQ IS NO: 34), MSAL-CDR1-1 (SEQ IS NO: 35), MSAL-CDR1-1c (SEQ IS NO: 36), HMVL1 (SEQ IS NO: 37), HMVL2 (SEQ IS NO: 38), HMVL3 (SEQ IS NO: 39), HMVL5 (SEQ IS NO: 40), HMVL8 (SEQ IS NO: 41), HMVL9 (SEQ IS NO: 42), HMVL10 (SEQ IS NO: 43), HMVL6 (SEQ IS NO: 44), HMVL4 (SEQ IS NO: 45), and HMVL7 (SEQ IS NO: 46)) used to construct the MSA1 and MSALVAC-1 variable regions.

On page 7, at line 13, please amend the paragraph beginning “Figures 12A-C.” as follows:

Figures 12A-C. (A) Nucleotide sequence for the MSA-63 epitope (SEQ ID NO: 19). (B) Amino acid sequence of the MSA-63 epitope encoded by the nucleotide sequence of Figure 12A (SEQ ID NO: 20). (C) MSA-63 oligonucleotides used to construct a modified variable region. Each oligo overlaps for five codons and transitions the entire sequence of Figure 12A (MSA1 (SEQ ID NO: 21), MSA2 (SEQ ID NO: 22), MSA3 (SEQ ID NO: 23), MSA4 (SEQ ID NO: 24), MSA5 (SEQ ID NO: 25), MSA6 (SEQ ID NO: 26), MSA7 (SEQ ID NO: 27)).

On page 7, at line 17, please amend the paragraph beginning “Figures 13A-C.” as follows:

Figures 13 A-C. (A) Nucleotide sequence for the SP-10 epitope (SEQ ID NO: 9). (B) Amino acid sequence of the SP-10 epitope encoded by the nucleotide sequence of Figure 13A (SEQ ID NO: 10). (C) Oligonucleotides of Sp-10 used to construct a modified variable region (SP1 (SEQ ID NO:11), SP2 (SEQ ID NO:12), SP3 (SEQ ID NO:13), SP4 (SEQ ID NO:15), SP5 (SEQ ID NO:17), and SP6 (SEQ ID NO:18)). SP3a (SEQ ID NO:14) and SP4a (SEQ ID NO:16) are modified to change the codons encoding certain cysteine residues to codons encoding alanine residues.

On page 7, at line 22, please amend the paragraph beginning “Figure 14.” as follows:

Figure 14. Oligonucleotides of LDH-C4 epitope sequence for construction of a modified variable region gene containing a LDH-C<sub>4</sub> (LDH1 (SEQ ID NO: 47), and LDH2 (SEQ ID NO: 48)).

On page 7, at line 24, please amend the paragraph beginning “Figure 15.” as follows:

Figure 15. Nucleotide (SEQ ID NO: 71) and amino acid (SEQ ID NO: 72) sequence of the consensus contraceptive light chain variable region.

On page 7, at line 26, please amend the paragraph beginning “Figure 16 A-B.” as follows:

Figure 16 A-B. (A) Sequences of oligos used in the construction of 2CAVHCOL1 (VHC1 (SEQ ID NO: 49), VHC2 (SEQ ID NO: 50), VHC3 (SEQ ID NO: 51), VHC4 (SEQ ID NO: 52), VHC5 (SEQ ID NO: 53), VHC6 (SEQ ID NO: 54), VHC7 (SEQ ID NO: 55), VHC8 (SEQ ID NO: 56), VHC9 (SEQ ID NO: 57), and VHC10 (SEQ ID NO: 58)). (B) Sequences of oligos used in the construction of 2CAVLCOL1 (VLC1 (SEQ ID NO: 59), VLC2 (SEQ ID NO: 60), VLC3 (SEQ ID NO: 61), VLC4 (SEQ ID NO: 62), VLC5 (SEQ ID NO: 63), VLC6 (SEQ ID NO: 64), VLC7 (SEQ ID NO: 65), VLC8 (SEQ ID NO: 66), VLC9 (SEQ ID NO: 67), VLC10 (SEQ ID NO: 68), VLC11 (SEQ ID NO: 69), and VLC12 (SEQ ID NO: 70)).

On page 38, at line 3, please amend the paragraph beginning “In order to confirm” as follows:

In order to confirm correct gene sequences of the engineered variable region genes and to eliminate the possibility of unwanted mutations generated during the construction procedure, DNA sequencing was performed using M13/pUC reverse primer (5'AACAGCTATGACCATG 3' (SEQ ID NO:1)) for the clones as well as PCR gene products using 5' end 20 base primer ( 5' GAATT CATGGCTTG GGTGTG 3' (SEQ ID NO: 2)) on automated ABI 377 DNA Sequencer. All clones were confirmed to contain correct sequences.

On page 40, at line 23, please amend the table beginning “Table 6.” as follows:

**Table 6.      Biotin-Labeled Peptides Derived from CDR Sequences of Mab 31.1**

**Peptide ID   Sequence**

COL311 L1	biotin-N-Thr-Ala-Lys-Ala-Ser-Gln-Ser-Val-Ser-Asn-Asp-Val-Ala ( <u>SEQ ID NO: 3</u> )
COL311 L2	biotin-N-Ile-Tyr-Tyr-Ala-Ser-Asn-Arg-Tyr-Thr ( <u>SEQ ID NO: 4</u> )
COL311 L3	biotin-N-Phe-Ala-Gln-Gln-Asp-Tyr-Ser-Ser-Pro-Leu-Thr ( <u>SEQ ID NO: 5</u> )
COL311 H1	biotin-N-Phe-Thr-Asn-Tyr-Gly-Met-Asn ( <u>SEQ ID NO: 6</u> )
COL311 H2	biotin-N-Ala-Gly-Trp-Ile-Asn-Thr-Tyr-Thr-Gly-Glu-Pro-Thr-Tyr-Ala-Asp-Asp-Phe-Lys-Gly ( <u>SEQ ID NO: 7</u> )
COL311 H3	biotin-N-Ala-Arg-Ala-Tyr-Tyr-Gly-Lys-Tyr-Phe-Asp-Tyr ( <u>SEQ ID NO: 8</u> )

On page 41, at line 25, please amend the paragraph beginning “The nucleotide and protein sequences” as follows:

The nucleotide and protein sequences of the SP-10 epitope are:

GAA TTC CAG CCT TCA GGT GAA CAT GGC TCC GGT GAA CAG CCT TCT  
GGT GAG CAG GCC TCG GGT GAA CAG CCT TCA GGT GAG CAC GCT TCA  
GGG GAA CAG GCT TCA GGT GCA CCA ATT TCA AGC ACA TCT ACA GGC

ACA ATA TTA AAT TGC TAC ACA TGT GCT TAT ATG AAT GAT CAA GGA  
AAA TGT CTT CGT GGA GAG GGA ACC TGC ATC ACT CAG AAT TC (SEQ  
ID NO: 9);

Gln Pro Ser Gly Glu His Gly Glu Gln Pro Ser Gly Glu Gln Ala Ser Gly Glu Gln Pro  
Ser gly Glu His Ala Ser Gly Glu Gln Ala Ser Gly Ala [Gln] Gln Ile Ser Ser Thr Ser  
Thr Gly Thr Ile Leu Asn Cys Tyr Thr Cys Ala Tyr Met Asn Asp Gln Gly Lys Cys Leu  
Arg Gly Glu Gly Thr Cys Ile Thr Gln Asn (SEQ ID NO: 10).

Beginning on page 41, at line 33, continuing to page 42, line 20, please amend  
the paragraph beginning “The replacement of an antibody's CDR” as follows:

The replacement of an antibody's CDR with another epitope is made  
easier by the fact that the variable region sequence of antibodies are relatively short,  
and are known. One is then able to synthetically generate a series of complementary  
oligonucleotides that, when annealed and ligated, reconstruct the entire coding region  
of variable region portion of the gene. In this manner, the CDR is replaced with  
sequences of the epitope of interest, in this example, SP-10. The following is a list of  
the sequences of the oligonucleotides designed for cloning SP-10 epitopes into the  
CDR:

**Oligo SP 1 (SEQ ID NO: 11):**

GAA TTC CAG CCT TCA GGT GAA CAT GGC TCC GGT GAA CAG CCT TCT  
GGT GAG CAG GCC TCG GGT GAA CAG CCT TAG,

**Oligo SP 2 (SEQ ID NO: 12):**

GTG AGC ACG CTT CAG GGG AAC AGC CTT CAG GTG CAC CAA TTT CAA  
GCA CAT CTA CAG GCA CAA TAT TAA ATT GCT,

**Oligo SP 3 (SEQ ID NO: 13):**

ACA CAT GTG CTT ATA TGA ATG ATC AAG GAA AAT GTC TTC GTG GAG  
AGG GAA CCT GCA TCA CTC AGA ATT C,

**Oligo SP 3a(3Cys-> Ala) (SEQ ID NO: 14):**

ACA CAG CAG CTT ATA TGA ATG ATC AAG GAA AAG CAC TTC GTG GAG  
AGG GAA CCG CAA TCA CTC AGA ATT C,

**Oligo SP 4 (SEQ ID NO: 15):**



peptides three amino acids in length, an oligonucleotide encoding residues 143 to 146 is synthesized. The second oligonucleotide synthesized encodes residues 146 to 148. The third encodes residues 148 to 150, and this continues until the entire epitope is covered in this fashion. The next oligonucleotide that is synthesized is four amino acid codons in length. It begins with residues 143 to 146, its second segment is equivalent to residues 145 to 148, its third segment corresponds to residues 147 to 150, and so on until the entire epitope is transitioned in this fashion. The next oligonucleotide synthesized contains five amino acid codons with two overlapping with the previous. For example, the first oligonucleotide encodes residues 143 to 147, and the second residues 146 to 150. This pattern continues until the entire epitope has been transitioned. The next construct encoding an epitope uses nucleotides for six amino acid codons with two overlapping with the previous codons as described *infra*.

On page 43, at line 24, please amend the paragraph beginning “In a specific example,” as follows:

In a specific example, oligomers have been designed which scan the entire length of the MSA-63 epitope and encode 15 amino acids. Each oligo overlaps with the previous one for the equivalent of five amino acids. MSA-63 oligos encoding 15 amino acids, with overlap of five amino acids each:

**MSA1:** GTC GGC AGC CTC CGA AGC AGC CCG CTC CAG AGC CCG CTG  
CTC CGA (SEQ ID NO: 21)

**MSA2:** AGC CCG CTG CTC CGA CCG CTC GTC CAG AGC AGC CTC TGC  
TTG CTG (SEQ ID NO: 22)

**MSA3:** AGC CTC TGC TTG CTG TTC CTC TTG CTG CGA TAC AGC TGC  
GGC GAC (SEQ ID NO: 23)

**MSA4:** TAC AGC TGC GGC GAC GGC AGC TGC AGC CGA CGA TAC TGC  
GAC TTG (SEQ ID NO: 24)

**MSA5:** CGA TAC TGC GAC TTG ACG GTG TGC ACG CGA ATG TAC TTG  
CTG CTG (SEQ ID NO: 25)

**MSA6:** ATG TAC TTG CTG CTG CGA TTC ACG GAC GCG CCG CTC CCG  
CAG ACG (SEQ ID NO: 26)

**MSA7:** CGA TTC ACG GAC GCG CCG CTC CCG CAG ACG TGC TGC GTC  
TTG AGC (SEQ ID NO: 27)



## CONTRACEPTIVE ANTIBODY VACCINES

### 1. FIELD OF THE INVENTION

5       The present invention relates to modified antibodies, and vaccine compositions thereof, that have one or more complementary determining regions that contain portions of sperm antigens, in which modified antibodies one or more variable region cysteine residues that form intrachain disulfide bonds have been replaced with amino acid residues that do not contain a sulfhydryl group and, therefore, do not form disulfide bonds. The present  
10 invention also relates to use of the vaccine compositions of the invention as a contraceptive.

### 2. BACKGROUND OF THE INVENTION

#### 2.1. IMMUNOGLOBULIN STRUCTURE

      The basic unit of immunoglobulin structure is a complex of four polypeptides --  
15 two identical low molecular weight or "light" chains and two identical high molecular weight or "heavy" chains, linked together by both noncovalent associations and by disulfide bonds. Each light and heavy chain of an antibody has a variable region at its amino terminus and a constant domain at its carboxyl terminus (Figure 1). The variable regions are distinct for each antibody and contain the antibody antigen binding site. Each variable  
20 domain is comprised of four relatively conserved framework regions and three regions of sequence hypervariability termed complementarity determining regions or CDRs (Figure 2). For the most part, it is the CDRs that form the antigen binding site and confer antigen specificity. The constant regions are more highly conserved than the variable domains, with slight variations due to haplotypic differences.

25       Based on their amino acid sequences, light chains are classified as either kappa or lambda. The constant region heavy chains are composed of multiple domains (CH1, CH2, CH3...CHx), the number depending upon the particular antibody class. The CH1 region is separated from the CH2 region by a hinge region which allows flexibility in the antibody. The variable region of each light chain aligns with the variable region of each heavy chain,  
30 and the constant region of each light chain aligns with the first constant region of each heavy chain. The CH2-CHx domains of the constant region of a heavy chain form an "Fc region" which is responsible for the effector functions of the immunoglobulin molecule, such as complement binding and binding to the Fc receptors expressed by lymphocytes, granulocytes, monocyte lineage cells, killer cells, mast cells and other immune effector  
35 cells.

As seen in Figure 3, the light and heavy chains of an IgG molecule form the variable region domain and the constant region domain. Each domain is composed of a sandwich of two parallel extended protein layers of about 100 amino acids in length which are connected by a single disulfide bond (See Roitt et al., Immunology, 3rd Edition, London; Mosby, 1993, p4.4 (Figure 3)). Each of the two extended protein layers of the domain, in turn, contains two "anti-parallel" adjacent strands which adopt a beta-sheet conformation. (See, e.g., Stryer, 1975, Biochemistry, WH Freeman and Co., p. 950). Each of the domains has a similar three-dimensional structure based on the immunoglobulin fold.

## 10                    2.2. IMMUNOTHERAPY AND ANTI-IDIOTYPE ANTIBODIES

In modern medicine, immunotherapy or vaccination has virtually eradicated diseases such as polio, tetanus, tuberculosis, chicken pox, measles, hepatitis, etc. The approach using vaccinations has exploited the ability of the immune system to prevent infectious diseases.

15                    Use of immunotherapy has also been explored for cancer therapy. The era of tumor immunology began with experiments by Prehn and Main, who showed that antigens on the methylcholanthrene (MCA)-induced sarcomas were tumor specific in that transplantation assays could not detect these antigens in normal tissue of the mice (Prehn et al., 1957, J. Natl. Cancer Inst. 18:79-778). This notion was confirmed by further experiments  
20 demonstrating that tumor specific resistance against MCA-induced tumors could be elicited in the autochthonous host, that is, the mouse in which the tumor originated (Klein et al., 1990, Cancer Res. 20:151-1572).

There are many reasons why immunotherapy is desired for use in cancer patients. First, if cancer patients are immunosuppressed in surgery, with anesthesia and subsequent  
25 chemotherapy, it may worsen the immunosuppression, then with appropriate immunotherapy in the preoperative period, this immunosuppression may be prevented or reversed. This could lead to fewer infectious complications and accelerated wound healing. Second, tumor bulk is minimal following surgery and immunotherapy is most likely to be effective in this situation. A third reason is the possibility that tumor cells are shed into the  
30 circulation at surgery and effective immunotherapy applied at this time can eliminate these cells.

There are two types of immunotherapy, the "active immunotherapy" and the "passive immunotherapy". In "active immunotherapy", an antigen is administered in the form of a vaccine, to a patient, so as to elicit a protective immune response. "Passive  
35 immunotherapy" involves the administration of antibodies to a patient without eliciting a concomitant immune response. When a specific antibody from one animal is injected as

an immunogen into a suitable second animal, the injected antibody will elicit an immune response. Antibody therapy is conventionally characterized as passive since the patient is not the source of the antibodies. However, the term passive is misleading because the patient can produce anti-idiotypic secondary antibodies which in turn provoke an immune  
5 response which is cross-reactive with the original antigen. Immunotherapy where the patient generates secondary antibodies is often more therapeutically effective than passive immunotherapy because the patient's own immune system continues to fight the cells bearing the particular antigen well after the initial infusion of antibody.

In an anti-idiotypic response, antibodies produced initially during an immune  
10 response or introduced into an organism will carry unique new epitopes to which the organism is not tolerant, and therefore will elicit production of secondary antibodies (termed "Ab2"), some of which are directed against the idiotype (*i.e.*, the antigen binding site) of the primary antibody (termed "Ab1"), *i.e.*, the antibody that was initially produced or introduced exogenously. These secondary antibodies or Ab2 likewise will have an  
15 idiotype, which will induce production of tertiary antibodies (termed "Ab3"), some of which will recognize the antigen binding site of Ab2, and so forth. This is known as the "network" theory. Some of the secondary antibodies will have a binding site which is an analog of the original antigen, and thus will reproduce the "internal image" of the original antigen. And, the tertiary or Ab3 antibodies that recognize this antigen binding site of the Ab2 antibody  
20 will also recognize the original antigen (Figure 4).

Therefore, anti-idiotypic antibodies have binding sites that are similar in conformation and charge to the antigen, and can elicit the same or greater response than that of the cancer antigen itself. Administration of an exogenous antibody that can elicit a strong anti-idiotypic response can thus serve as an effective vaccine, by maintaining a  
25 constant immune response.

To date, anti-idiotypic vaccines have comprised murine antibodies because the anti-idiotypic response occurs as part of the typical human anti-mouse antibody (HAMA) response. A strong anti-idiotypic cascade has been observed when Ab1 has been structurally damaged (Madiyalakan et al., 1995, *Hybridoma* 14:199-203), rendering the  
30 antibody more foreign. There has been direct administration to the subject of exogenously produced anti-idiotypic antibodies that are raised against the idiotype of an anti-tumor antibody (U.S. Patent No. 4,918,14). After administration, the subject's body will produce anti-antibodies which not only recognize these anti-idiotypic antibodies, but also recognize the original tumor epitope, thereby directing complement activation and other immune  
35 system responses to a foreign entity to attack the tumor cell that expresses the tumor epitope.



second immunoglobulin molecule, said second immunoglobulin molecule being capable of immunospecifically binding (*i.e.*, specific binding of the immunoglobulin to its antigen as determined by any method known in the art for determining antibody-antigen binding, which excludes non-specific binding but not necessarily cross-reactivity with other  
 5 antigens) an antigen or having a CDR that contains a portion of an antigen, said one or more amino acid substitutions being the substitution of one or more amino acid residues that do not have a sulfhydryl group at one or more positions corresponding to one or more cysteine residues that form a disulfide bond in said second immunoglobulin molecule. In preferred  
 10 embodiments, the second immunoglobulin molecule contains a CDR that contains a portion of an antigen of a cell or protein involved in reproductive function, preferably sperm antigens, more preferably the sperm antigens SP-10, LDH-C<sub>4</sub>, or MSA-63.

The invention further provides methods of eliciting an anti-idiotypic response in a subject by administering the modified immunoglobulins of the invention. In particular, the modified immunoglobulins of the invention can be used as contraceptives, either in males  
 15 or, preferably in females, specifically by administering an immunoglobulin molecule of the invention, which immunoglobulin molecule was derived (*i.e.*, by modification according to the invention to replace one or more variable region cysteine residues that form an intrachain disulfide bond with an amino acid residue that does not contain a sulfhydryl group) from an immunoglobulin molecule that contains a CDR that contains a portion of an  
 20 antigen of a protein or cell associated with reproductive function, preferably a sperm antigen.

The invention also provides methods of producing the modified immunoglobulin molecules of the invention and vaccine compositions containing the modified immunoglobulin molecules of the invention.

25

#### 4. DESCRIPTION OF FIGURES

Figure 1. A schematic diagram showing the structure of the light and heavy chain of an immunoglobulin molecule, each chain consisting of a variable region positioned at the amino terminal region (H<sub>2</sub>N-) and a constant region positioned at a carboxyl terminal region  
 30 (-COOH).

Figure 2. A schematic diagram of an IgG showing the four framework regions (FR1, FR2, FR3 and FR4) and three complementarity determining regions (CDR1, CDR2 and CDR3) in the variable regions of the light and heavy chains (labeled as V<sub>L</sub> and V<sub>H</sub>, respectively). The constant region domains are indicated as C<sub>L</sub> for the light chain constant  
 35 domain and CH<sub>1</sub>, CH<sub>2</sub> and CH<sub>3</sub> for the three domains of the heavy chain constant region. Fab indicates the portion of the antibody fragment which includes the variable region

domains of both light and heavy chains and the  $C_L$  and  $CH_1$  domains.  $F_c$  indicates the constant region fragment containing the  $CH_2$  and  $CH_3$  domains.

Figure 3. A schematic diagram of an antibody structure as shown in Figure 2, but drawn to emphasize that each domain (the loop structures labeled as  $V_L$ ,  $V_H$ ,  $C_L$ ,  $CH_1$ ,  $CH_2$ , and  $CH_3$ , respectively) is structurally defined by a disulfide bond (indicated with darkest lines) that maintains the three-dimensional structure (Roitt et al., *Immunology*, Second Edition, London: Gower Medical Publishing, 1989, p 5.3).

Figure 4. A schematic diagram showing the development of internal image bearing anti-idiotypic antibodies (Ab2) and anti-anti-idiotypic antibodies (Ab3) from idiotype antibodies (Ab1) directed against an antigen of a tumor cell in an antiidiotypic cascade.

Figure 5. Modification of the variable region of an immunoglobulin by replacing cysteine residues in the variable regions with alanine residues to remove an intrachain disulfide bond.  $CH_1$ ,  $CH_2$  and  $CH_3$  are constant regions.  $V_H$  is the heavy chain variable region and  $V_L$  is the light chain variable region.

Figures 6A-C. (A). The structure of the expression vector pMRRO10.1, which contains a human kappa light chain constant region sequence. (B). The structure of the expression vector pGamma1 that contains a sequence encoding a human IgG1 constant region ( $CH_1$ ,  $CH_2$ ,  $CH_3$ ) heavy chain and hinge region sequences. (C) The structure of the expression vector pNEPuDGV which contains a sequence encoding the kappa constant domain of the light chain and the constant domain and hinge region of the heavy chain. For all three vectors see Bebbington et al., 1991, *Methods in Enzymology* 2:136-145.

Figures 7A and B. (A) The amino acid sequence and corresponding nucleotide sequence for the consensus light chain variable region ConVL1. (B) The amino acid and corresponding nucleotide sequences for the consensus heavy chain variable region ConVH1.

Figure 8. A schematic diagram of the general steps that were followed for the assembly of an engineered gene encoding the synthetic modified antibody specific to human colon cancer antigen.

Figure 9. Dot blot showing the result of an assay for the competition of binding of the antibody derived from mAB31.1, but not having the cysteine to alanine changes with the same antibody which is biotin labeled to an antigen preparation derived from LS-174 T-cells. The concentration of the unlabeled antibody is indicated as nM unlabeled antibody. The "blk" lane has no antigen.

Figures 10A-D. (A) Results of competition binding assay of the biotin-labeled anti-colon carcinoma cell antibody to LS-174T cells in the presence of antisera from mice vaccinated with vehicle alone, control antibody that binds the colon carcinoma cell antibody

but has not been modified, and peptides CDR1, CDR2, CDR3, CDR4, CDR5, and CDR6, having the CDR sequences containing the bradykinin receptor binding site expressed as percent of control binding to LS-174T cells. (B). Results of competition binding assays of the biotin-labeled anti-colon carcinoma cell antibody to LS-174T cells in the presence of  
5 antisera from mice vaccinated with vehicle alone, control antibody that binds the colon carcinoma cell antibody, but has not been modified, 2CAVHCOL1, and 2CAVLCOL1. (C) Diagram showing the binding of a biotin-labeled (indicated by the "b") antibody (inverted Y) to antigen (solid triangles). (D) Diagram showing the inhibition of binding of the biotin-labeled (indicated by the "b") antibody (inverted Y) by anti-idiotypic antibodies (solid  
10 arrows) to antigen (solid triangles).

Figure 11. Nucleotide sequences of the oligonucleotides used to construct the MSA1 and MSALVAC-1 variable regions.

Figures 12A-C. (A) Nucleotide sequence for the MSA-63 epitope. (B) Amino acid sequence of the MSA-63 epitope encoded by the nucleotide sequence of Figure 12A. (C)  
15 MSA-63 oligonucleotides used to construct a modified variable region. Each oligo overlaps for five codons and transitions the entire sequence of Figure 12A.

Figures 13 A-C. (A) Nucleotide sequence for the SP-10 epitope. (B) Amino acid sequence of the SP-10 epitope encoded by the nucleotide sequence of Figure 13A. (C) Oligonucleotides of Sp-10 used to construct a modified variable region. SP3a and SP4a are  
20 modified to change the codons encoding certain cysteine residues to codons encoding alanine residues.

Figure 14. Oligonucleotides of LDH-C4 epitope sequence for construction of a modified variable region gene containing a LDH-C<sub>4</sub>.

Figure 15. Nucleotide and amino acid sequence of the consensus contraceptive light  
25 chain variable region.

Figure 16 A-B. (A) Sequences of oligos used in the construction of 2CAVHCOL1. (B) Sequences of oligos used in the construction of 2CAVLCOL1.

## 5. DETAILED DESCRIPTION OF THE INVENTION

30 The present invention provides modified immunoglobulins (particularly antibodies and functionally active fragments, derivatives, and analogs thereof) that can be used as contraceptive vaccines. Specifically, these antibodies have one or more complementarity determining regions (CDRs) that contain a portion of an antigen of a cell or protein involved in reproductive function, preferably a sperm antigen. In addition, these antibodies  
35 have been engineered to elicit a stronger immune response, particularly a stronger anti-idiotypic response, than the corresponding unmodified immunoglobulins. In particular, the

modified immunoglobulins of the invention are immunoglobulins that are modified to decrease the conformational constraints on one variable region of the immunoglobulin molecule, preferably, such that at least one of the cysteines that participates in forming an intrachain disulfide bond in the variable region of the immunoglobulin has been replaced  
5 with an amino acid residue that does not have a sulfhydryl group and, therefore, does not form a disulfide bond, thereby decreasing the conformational constraints of at least one of the variable regions of the immunoglobulin (Figure 5).

The invention also provides vaccine compositions containing the modified immunoglobulin molecules of the invention. Additionally, the invention provides methods  
10 of generating an anti-idiotypic response in a subject by administration of the modified immunoglobulin molecules of the invention.

In specific embodiments, the invention provides methods of contraception by administration of a modified immunoglobulin molecule of the invention which, in its unmodified state, is capable of immunospecifically binding an antigen of a protein or cell  
15 associated with reproductive function, such as a sperm antigen. Administration of the modified immunoglobulin elicits an anti-idiotypic reaction in the subject, leading to the production, by the subject, of antibodies specific for the particular antigen.

For clarity of disclosure, and not by way of limitation, the detailed description of the invention is divided into the subsections which follow.

20

### **5.1. MODIFIED ANTIBODIES**

The modified immunoglobulins, particularly antibodies, of the invention are immunoglobulins that, at least in the unmodified state, can immunospecifically bind an antigen of a cell or protein associated with reproductive function, and have been modified to  
25 enhance their ability to elicit an anti-idiotypic response. Such immunoglobulins are modified to reduce the conformational constraints on a variable region of the immunoglobulin, *e.g.*, by removing or reducing intrachain or interchain disulfide bonds. Specifically, the invention provides a first immunoglobulin molecule that comprises a variable region and that is identical, except for one or more amino acid substitutions in the  
30 variable region, to a second immunoglobulin molecule, the second immunoglobulin molecule being capable of immunospecifically binding an antigen, the amino acid substitutions being the substitution of one or more amino acid residues that do not have a sulfhydryl group at one or more positions corresponding to one or more cysteine residues that form a disulfide bond in said second immunoglobulin molecule. (See, co-pending  
35 United States Patent Application Serial No., entitled "Modified Antibodies With Enhanced Ability To Elicit An Anti-Idiotypic Response", filed November 13, 1998 (attorney docket

no. 6750-015), which is incorporated by reference herein in its entirety. The invention also provides nucleic acids containing a nucleotide sequence encoding a modified immunoglobulin of the invention.

Identifying the cysteine residues that form a disulfide bond in a variable region of a particular antibody can be accomplished by any method known in the art. For example, but not by way of limitation, it is well known in the art that the cysteine residues that form intrachain disulfide bonds are highly conserved among antibody classes and across species. Thus, the cysteine residues that participate in disulfide bond formation can be identified by sequence comparison with other antibody molecules in which it is known which residues form a disulfide bond.

Table 1 provides a list of the positions of disulfide bond forming cysteine residues for a number of antibody molecules.

Table 1 (derived from Kabat et al, 1991, sequences of Proteins of Immunological Interest, 5th Ed., U.S. Department of Health and Human Services, Bethesda, Maryland).

Species	Variable domain	Subgroup	Disulfide bond-forming cysteines (positions)
Human	kappa light	I	23,88
Human	kappa light	II	23,88
Human	kappa light	III	23,88
Human	kappa light	IV	23,88
Human	lambda light	I	23,88
Human	lambda light	II	23,88
Human	lambda light	III	23,88
Human	lambda light	IV	23,88
Human	lambda light	V	23,88
Human	lambda light	VI	23,88
Mouse	kappa light	I	23,88
Mouse	kappa light	II	23,88
Mouse	kappa light	III	23,88
Mouse	kappa light	IV	23,88
Mouse	kappa light	V	23,88
Mouse	kappa light	VI	23,88
Mouse	kappa light	VII	23,88
Mouse	kappa light	Miscellaneous	23,88
Mouse	lambda light		23,88
Chimpanzee	lambda light		23,88
Rat	kappa light		23,88
Rat	lambda light		23,88
Rabbit	kappa light		23,88
Rabbit	lambda light		23,88



Position numbers enclosed by ( ) indicate that the protein was not sequenced to that position, but the residue is inferred by comparison to known sequences.

Notably, for all of the antibody molecules listed in Table 1, the cysteine residues that form the intrachain disulfide bonds are the residues at positions 23 and 88 of the light chain variable domain and the residues at positions 22 and 92 of the heavy chain variable domain. The position numbers refer to the residue corresponding to that residue in the consensus sequences as defined in Kabat, (1991, Sequences of Proteins of Immunological Interest, 5th Ed., U.S. Department of Health and Human Services, Bethesda, Maryland) or as indicated in the heavy and light chain variable region sequences depicted in Figures 7A and B, respectively ("corresponding" means as determined by aligning the particular antibody sequence with the consensus sequence or the heavy or light chain variable region sequence depicted in Figure 7A or B).

Accordingly, in one embodiment of the invention, the modified immunoglobulin molecule is an antibody in which the residues at positions 23 and/or 88 of the light chain are substituted with an amino acid residue that does not contain a sulfhydryl group and/or the residues at positions 22 and/or 92 of the heavy chain are substituted with an amino acid residue that does not contain a sulfhydryl group.

In the modified immunoglobulin of the invention, the amino acid residue that substitutes for the disulfide bond forming cysteine residue is any amino acid residue that does not contain a sulfhydryl group, *e.g.*, alanine, arginine, asparagine, aspartate (or aspartic acid), glutamine, glutamate (or glutamic acid), glycine, histidine, isoleucine, leucine, lysine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine or valine. In a preferred embodiment, the cysteine residue is replaced with a glycine, serine, threonine, tyrosine, asparagine, or glutamine residue, most preferably, with an alanine residue.

Additionally, the disulfide bond forming cysteine residue may be replaced by a nonclassical amino acid or chemical amino acid analog that does not contain a sulfhydryl group (for example, but not by way of limitation, using routine protein synthesis methods). Non-classical amino acids include, but are not limited, to the D-isomers of the common amino acids,  $\alpha$ -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-aminobutyric acid,  $\gamma$ -Abu,  $\epsilon$ -Ahx, -amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine,  $\beta$ -alanine, fluoro-amino acids, designer amino acids such as  $\beta$ -methyl amino acids, C $\alpha$ -methyl amino acids, N $\alpha$ -methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary). In an alternative embodiment, the disulfide bond forming residue is deleted.



substituted by another amino acid of a similar polarity which acts as a functional equivalent. Substitutes for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid.

The modified immunoglobulin is derived from an antibody that has one or more CDRs containing a portion of an antigen of a cell or protein associated with reproductive function. In specific embodiments, the antigen is a sperm antigen, preferably SP-10. Other antigens include lactate dehydrogenase LDH-C4, SP-17, PH-20, FA-1, FA-2, PH-30, RSA, HAS-63, MSA-63, or zona pellucida proteins ZP1, ZP2, and ZP3 (see, e.g., Freemerman et al., 1993, *Molecular Reproduction and Development* 34:140-148; Herr et al., 1990, *Biol. Reproduction* 42:181-193; O'Hern et al., 1995, *Biol. Reproduction* 52:331-339; Anderson et al., 1986, *J. Reprod. Immunol.* 10:231-257; Wright et al., 1990, *Biology of Reproduction* 42:693-701; Lea et al., 1997, *Fertility and Sterility* 67:355-361; O'Hern et al., Elsevier Science Ltd. 16:1761-1766; Kerr, 1995, *Reprod. Fertil. Dev.* 7:825-830; Kaul et al., 1996, *Reprod. Fertil. Dev.* 50:127-134; Liu et al., 1990, *Molecular Reproduction and Development* 25:302-308; Bambra, 1992, *Scand. J. Immunol.* 11:118-122) or another antigen of a cell or protein associated with reproductive function, for example but not limited to gonadotropin-releasing hormone, any gonadotropin, prostaglandin F2 alpha, oxytocin, and gonadotropin receptors.

The immunoglobulin molecules of the invention can be of any type, class, or subclass of immunoglobulin molecules. In a preferred embodiment, the immunoglobulin molecule is an antibody molecule, more preferably of a type selected from the group consisting of IgG, IgE, IgM, IgD and IgA, most preferably is an IgG molecule. Alternatively, the immunoglobulin molecule is a T cell receptor, a B cell receptor, a cell-surface adhesion molecule such as the co-receptors CD4, CD8, or CD19, or an invariant domain of an MHC molecule.

The modified immunoglobulin can be derived from any naturally occurring antibody, preferably a monoclonal antibody, or can be derived from a synthetic or engineered antibody. Specifically, the modified immunoglobulin molecules are derived from an antibody in which a portion of an antigen of a cell or protein associated with reproductive function is inserted into or replaces all or a portion of one of the CDRs in the variable region, for example as described in co-pending United States Patent application

Serial No., entitled "Immunoglobulin Molecules Having A Synthetic Variable Region And Modified Specificity", by Burch, filed November 13, 1998 (attorney docket no. 6750-016), which is incorporated by reference herein in its entirety.

In particular, the synthetic antibodies are antibodies that in which at least one of the  
 5 CDRs of the antibody contains an antigen of a cell or protein associated with reproductive function. In one aspect of the invention, the amino acid sequence of the antigen is not found naturally within the CDR. One or more CDRs may also contain a binding site for a cell or protein involved in reproductive function.

The amino acid sequence of the binding site may be identified by any method  
 10 known in the art. For example, in some instances, the sequence of a member of a binding pair has already been determined to be directly involved in binding the other member of the binding pair. In this case, such a sequence can be used to construct the CDR of a synthetic antibody that specifically recognizes the other member of the binding pair. If the amino acid sequence for the binding site in the one member of the binding pair for the other  
 15 member of the binding pair is not known, it can be determined by any method known in the art, for example, but not limited to, molecular modeling methods or empirical methods, *e.g.*, by assaying portions (*e.g.*, peptides) of the member for binding to the other member, or by making mutations in the member and determining which mutations prevent binding.

The binding pair can be any two molecules, including proteins, nucleic acids,  
 20 carbohydrates, or lipids, that interact with each other, although preferably the binding partner from which the binding site is derived is a protein molecule. In preferred embodiments, the modified immunoglobulin contains a binding sequence for a cancer antigen, an infectious disease antigen, a cellular receptor for a pathogen, or a receptor or ligand that participates in a receptor-ligand binding pair.

25 In specific embodiments, the binding pair is a protein-protein interaction pair which is either homotypic interaction (*i.e.*, is the interaction between two of the same proteins) or a heterotypic interaction (*i.e.*, is the interaction between two different proteins).

The synthetic antibody may be built upon (*i.e.*, the binding site sequences inserted into the CDR of) the sequence of a naturally occurring or previously existing antibody or  
 30 may be synthesized from known antibody consensus sequences, such as the consensus sequences for the light and heavy chain variable regions in Figures 7A and B, or any other antibody consensus or germline (*i.e.*, unrecombined genomic sequences) sequences (*e.g.*, those antibody consensus and germline sequences described in Kabat et al., 1991, Sequences of Proteins of Immunological Interest, 5<sup>th</sup> edition, NIH Publication No. 91-3242,  
 35 pp 2147-2172).

Each antibody molecule has six CDR sequences, three on the light chain and three on the heavy chain, and five of these CDRs are germline CDRs (*i.e.*, are directly derived from the germline genomic sequence of the animal, without any recombination) and one of the CDRs is a non-germline CDR (*i.e.*, differs in sequence from the germline genomic sequence of the animal and is generated by recombination of the germline sequences). Whether a CDR is a germline or non-germline sequence can be determined by sequencing the CDR and then comparing the sequence with known germline sequences, *e.g.*, as listed in Kabat et al. (1991, Sequences of Proteins of Immunological Interest, 5<sup>th</sup> edition, NIH Publication No. 91-3242, pp 2147-2172). Significant variation from the known germline sequences indicates that the CDR is a non-germline CDR. Accordingly, the CDR that contains the amino acid sequence of the binding site or antigen is a germline CDR or, alternatively, is a non-germline CDR.

The binding site or antigen sequence can be inserted into any of the CDRs of the antibody, and it is within the skill in the art to insert the binding site into different CDRs of the antibody and then screen the resulting modified antibodies for the ability to bind to the particular member of the binding pair, *e.g.* as discussed in Section, *infra*, or to elicit an immune response against the antigenic site, *e.g.*, as described in Section, *infra*. Thus, one can determine which CDR optimally contains the binding site or antigen. In specific embodiments, a CDR of either the heavy or light chain variable region is modified to contain the amino acid sequence of the binding site or antigen. In another specific embodiment, the modified antibody contains a variable domain in which the first, second or third CDR of the heavy variable region or the first, second or third CDR of the light chain variable region contains the amino acid sequence of the binding site or antigen. In another embodiment of the invention, more than one CDR contains the amino acid sequence of the binding site or antigen or more than one CDR each contains a different binding site for the same molecule or contains a different binding site for a different molecule. In particular, embodiments, two, three, four, five or six CDRs have been engineered to contain a binding site for the first member of the binding pair. In a preferred embodiment, one of the CDRs contains a portion of one sperm antigen and another CDR contains a portion of a second sperm antigen, more particularly, where one sperm antigen is SP-10 and the other sperm antigen is MSA-63 or LHD-C<sub>4</sub>.

In specific embodiments of the invention, the binding site or antigen amino acid sequence is either inserted into the CDR without replacing any of the amino acid sequence of the CDR itself or, alternatively, the binding site or antigen amino acid sequence replaces all or a portion of the amino acid sequence of the CDR. In specific embodiments, the



first CDR of the heavy chain, H1, the CDR is 5 to 7 amino acid residues; if it is the second CDR of the heavy chain, H2, the CDR is 9 to 12 amino acid residues; and if it is the third CDR of the heavy chain, H3, the CDR is 2 to 25 amino acid residues. In other specific embodiments, the CDR containing the binding site is 5-10, 5-15, 5-20, 11-15, 11-20, 11-25, or 16-25 amino acids in length. In other embodiments, the CDR containing the binding site is at least 5, 10, 15, or 20 amino acids or is no more than 10, 15, 20, 25, or 30 amino acids in length.

After constructing antibodies containing modified CDRs, the modified antibodies can be further altered and screened to select an antibody having higher affinity or specificity. Antibodies having higher affinity or specificity for the target antigen may be generated and selected by any method known in the art. For example, but not by way of limitation, the nucleic acid encoding the synthetic modified antibody can be mutagenized, either randomly, *i.e.*, by chemical or site-directed mutagenesis, or by making particular mutations at specific positions in the nucleic acid encoding the modified antibody, and then screening the antibodies exposed from the mutated nucleic acid molecules for binding affinity for the target antigen. Screening can be accomplished by testing the expressed antibody molecules individually or by screening a library of the mutated sequences, *e.g.*, by phage display techniques (see, *e.g.*, U. S. Patent Nos. 5,223,409; 5,403,484; and 5,571,698, all by Ladner et al; PCT Publication WO 92/01047 by McCafferty et al. or any other phage display technique known in the art).

In specific embodiments, the invention provides a functionally active fragment, derivative or analog of the modified immunoglobulin molecules of the invention. Functionally active means that the fragment, derivative or analog is able to elicit anti-idiotype antibodies (*i.e.*, tertiary antibodies or Ab3 antibodies) that recognize the same antigen that the antibody from which the fragment, derivative or analog is derived recognized (*e.g.*, as determined by the methods described in Section 5.4, *infra*). Specifically, in a preferred embodiment, the antigenicity of the idiotype of the immunoglobulin molecule may be enhanced by deletion of framework and CDR sequences that are N-terminal to the particular CDR sequence that specifically recognizes the antigen. To determine which CDR sequences bind the antigen, synthetic peptides containing the CDR sequences can be used in binding assays with the antigen by any binding assay method known in the art. Accordingly, in a preferred embodiment, the invention includes modified immunoglobulin molecules that have one disulfide bond forming cysteine residue in a variable region domain replaced with an amino acid residue that does not contain a sulfhydryl group and in which a portion of that variable domain has been deleted N-terminal to the CDR sequence that recognizes the antigen.

Other embodiments of the invention include fragments of the modified antibodies of the invention such as, but not limited to, F(ab')<sub>2</sub> fragments, which contain the variable region, the light chain constant region and the CH1 domain of the heavy chain can be produced by pepsin digestion of the antibody molecule, and Fab fragments, which can be generated by reducing the disulfide bridges of the F(ab')<sub>2</sub> fragments. The invention also provides heavy chain and light chain dimers of the modified antibodies of the invention, or any minimal fragment thereof such as Fvs or single chain antibodies (SCAs) (e.g., as described in U.S. Patent 4,946,778; Bird, 1988, *Science* 242:423-42; Huston et al., 1988, *Proc. Natl. Acad. Sci. USA* 85:5879-5883; and Ward et al., 1989, *Nature* 334:544-54), or any other molecule with the same specificity as the modified antibody of the invention.

Techniques have been developed for the production of "chimeric antibodies" (Morrison et al., 1984, *Proc. Natl. Acad. Sci.* 81:851-855; Neuberger et al., 1984, *Nature* 312:604-608; Takeda et al., 1985, *Nature* 314:452-454) by splicing the genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine monoclonal antibody and a constant domain from a human immunoglobulin, e.g., humanized antibodies.

In a preferred embodiment, the modified immunoglobulin of the invention is a humanized antibody, more preferably an antibody having a variable domain in which the framework regions are from a human antibody and the CDRs are from an antibody of a non-human animal, preferably a mouse (see, International Patent Application No. PCT/GB8500392 by Neuberger et al. and Celltech Limited).

CDR grafting is another method of humanizing antibodies. It involves reshaping murine antibodies in order to transfer full antigen specificity and binding affinity to a human framework (Winter et al. U.S. Patent No. 5,225,539). CDR-grafted antibodies have been successfully constructed against various antigens, for example, antibodies against IL-2 receptor as described in Queen et al., 1989 (*Proc. Natl. Acad. Sci. USA* 86:10029); antibodies against cell surface receptors-CAMPATH as described in Riechmann et al. (1988, *Nature*, 332:323); antibodies against hepatitis B in Cole et al. (1991, *Proc. Natl. Acad. Sci. USA* 88:2869); as well as against viral antigens-respiratory syncytial virus in Tempest et al. (1991, *Bio-Technology* 9:267). CDR-grafted antibodies are generated in which the CDRs of the murine monoclonal antibody are grafted into a human antibody. Following grafting, most antibodies benefit from additional amino acid changes in the framework region to maintain affinity, presumably because framework residues are necessary to maintain CDR conformation, and some framework residues have been

demonstrated to be part of the antigen binding site. However, in order to preserve the framework region so as not to introduce any antigenic site, the sequence is compared with established germline sequences followed by computer modeling.

In other embodiments, the invention provides fusion proteins of the modified immunoglobulins of the invention (or functionally active fragments thereof), for example in which the modified immunoglobulin is fused via a covalent bond (*e.g.*, a peptide bond), at either the N-terminus or the C-terminus to an amino acid sequence of another protein (or portion thereof, preferably an at least 10, 20 or 50 amino acid portion of the protein) that is not the modified immunoglobulin. Preferably the modified immunoglobulin, or fragment thereof, is covalently linked to the other protein at the N-terminus of the constant domain. In preferred embodiments, the invention provides fusion proteins in which the modified immunoglobulin is covalently linked to IL-2, IL-4, IL-5, IL-6, IL-7, IL-10,  $\gamma$ -interferon, MHC derived peptide, G-CSF, a porin, TNF, NK cell antigens, or cellular endocytosis receptor.

The modified immunoglobulins of the invention include analogs and derivatives that are either modified, *i.e.*, by the covalent attachment of any type of molecule as long as such covalent attachment does not prevent the modified immunoglobulin from generating an anti-idiotypic response (*e.g.*, as determined by any of the methods described in Section 5.5, *infra*). For example, but not by way of limitation, the derivatives and analogs of the modified immunoglobulins include those that have been further modified, *e.g.*, by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Additionally, the analog or derivative may contain one or more non-classical amino acids, *e.g.*, as listed above in this Section.

Methods of producing the modified immunoglobulins, and fragments, analogs, and derivatives thereof, are described in Section 5.4, *infra*.

## 30 5.2. CONTRACEPTIVE METHODS

The present invention provides methods of contraception by eliciting production of anti-idiotypic antibodies and anti-anti-idiotypic antibodies in a subject by the administration of a therapeutic (termed herein "Therapeutic"). Such Therapeutics include the modified immunoglobulins of the invention, and functionally active fragments, analogs, and derivatives thereof (*e.g.*, as described in Section 5.1, *supra*), and nucleic acids encoding the

modified antibodies of the invention, and functionally active fragments and derivatives thereof (*e.g.*, as described in Section 5.1, *supra*).

Generally, administration of products of a species origin or species reactivity that is the same species as that of the subject is preferred. Thus, in a preferred embodiment, the methods of the invention use a modified antibody that is derived from a human antibody; in other embodiments, the methods of the invention use a modified antibody that is derived from a chimeric or humanized antibody.

Specifically, vaccine compositions (*e.g.*, as described in Section 5.3, *infra*) containing the modified antibodies of the invention are administered to the subject to elicit the production of an antibody (*i.e.*, the anti-idiotypic antibody or Ab2) that specifically recognizes the idiotype of the modified antibody, the Ab2, in turn, elicits the production anti-anti-idiotypic antibodies (Ab3) that specifically recognize the idiotype of Ab2, such that these Ab3 antibodies have the same or similar binding specificity as the modified antibody.

The invention provides methods of administering the modified antibodies of the invention to elicit an anti-idiotypic response, *i.e.*, to generate Ab2 and Ab3 type antibodies. Alternatively, the invention provides methods of administering the modified antibodies of the invention to one subject to generate Ab2 antibodies, isolating the Ab2 antibodies, and then administering the Ab2 antibodies to a second subject to generate Ab3 type antibodies in that second subject.

Accordingly, the invention provides a method of generating an anti-idiotypic response in a subject comprising administering an amount of first immunoglobulin molecule (or functionally active fragment, analog, or derivative thereof) sufficient to induce an anti-idiotypic response, said first immunoglobulin comprising a variable region and being identical, except for one or more amino acid substitutions in said variable region, to a second immunoglobulin molecule, said second immunoglobulin molecule being capable of immunospecifically binding an antigen, said one or more amino acid substitutions being the substitution of an amino acid residue that does not have a sulfhydryl group at one or more positions corresponding to one or more cysteine residues that form a disulfide bond in said second immunoglobulin molecule. In another embodiment, the method further provides isolating the anti-idiotypic antibody that recognizes the idiotype of said second immunoglobulin molecule, and administering to a second subject the anti-idiotypic antibody.

Modified immunoglobulins capable of inhibiting the gamete interaction *i.e.*, of eggs and sperm are preferably employed. The key to this method of contraception is to either immunologically regulate molecules involved in reproduction or to inhibit fertilization. Such contraceptive vaccines target reproductive hormone or receptor-specific antigens or gamete-specific antigens. The goal is to elicit an immune response which targets



Reprod. Fertil Dev. 50:127-134; Liu et al., 1990, Molecular Reproduction and Development 25:302-308; Bambra, 1992, Scand. J. Immunol. 11:118-122).

The invention also includes contraceptive methods whereby a modified immunoglobulin of the invention is administered in conjunction with use of another  
5 contraceptive method, such as, but not limited to, barrier methods such as the use of condoms or diaphragms or cervical caps, or intravaginal use of contraceptive compounds such as, but not limited to, non-oxynol-9, intrauterine devices, birth control pills or implants, etc.

The invention also includes administrations of anti-anti-idiotypic antibodies against a  
10 modified immunoglobulin of the invention to acutely neutralize the contraceptive activity of the modified immunoglobulin.

The methods and vaccine compositions of the present invention may be used to elicit a humoral and/or a cell-mediated response against a modified immunoglobulin in a subject. In one specific embodiment, the methods and compositions of the invention elicit a  
15 humoral response in a subject. In another specific embodiment, the methods and compositions of the invention elicit a cell-mediated response in a subject. In a preferred embodiment, the methods and compositions of the invention elicit both a humoral and a cell-mediated response.

The subjects to which the present invention is applicable may be any mammalian or  
20 vertebrate species, which include, but are not limited to, cows, horses, sheep, pigs, fowl (e.g., chickens), goats, cats, dogs, hamsters, mice, rats, monkeys, rabbits, chimpanzees, and humans. In a preferred embodiment, the subject is a human.

#### 25 **5.2.1. GENE THERAPY**

Gene therapy may be used by administering a nucleic acid containing a nucleotide sequence encoding the modified immunoglobulin of the invention as a contraceptive. In this embodiment of the invention, the therapeutic nucleic acid encodes a sequence that produces intracellularly (without a leader sequence) or intercellularly (with a leader  
30 sequence), a modified immunoglobulin.

For general reviews of the methods of gene therapy, see Goldspiel et al., 1993, *Clinical Pharmacy* 12:488-505; Wu and Wu, 1991, *Biotherapy* 3:87-95; Tolstoshev, 1993, *Ann. Rev. Pharmacol. Toxicol.* 32:573-596; Mulligan, 1993, *Science* 260:926-932; and Morgan and Anderson, 1993, *Ann. Rev. Biochem.* 62:191-217). Methods commonly known  
35 in the art of recombinant DNA technology which can be used are described in Ausubel et al. (eds.), 1993, *Current Protocols in Molecular Biology*, John Wiley & Sons, NY; Kriegler,



those described in Marasco et al. (Marasco et al., 1993, *Proc. Natl. Acad. Sci. USA* 90:7889-7893). Adenoviruses are other viral vectors that can be used in gene therapy. Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are liver, the  
5 central nervous system, endothelial cells, and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing cells. Kozarsky and Wilson, 1993, *Current Opinion in Genetics and Development* 3:499-503 present a review of adenovirus-based gene therapy. Bout et al., 1994, *Human Gene Therapy* 5:3-10 demonstrated the use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys. Other  
10 instances of the use of adenoviruses in gene therapy can be found in Rosenfeld et al., 1991, *Science* 252:431-434; Rosenfeld et al., 1992, *Cell* 68:143-155; and Mastrangeli et al., 1993, *J. Clin. Invest.* 91:225-234. Adeno-associated virus (AAV) has also been proposed for use in gene therapy (Walsh et al., 1993, *Proc. Soc. Exp. Biol. Med.* 204:289-300).

The form and amount of therapeutic nucleic acid envisioned for use depends on the  
15 type of disease and the severity of its desired effect, patient state, etc., and can be determined by one skilled in the art.

### 5.3. VACCINE FORMULATIONS AND ADMINISTRATION

The invention also provides vaccine formulations containing Therapeutics of the  
20 invention, which vaccine formulations are suitable for administration to elicit a protective immune (humoral and/or cell mediated) response against certain antigens, *e.g.*, for the contraceptive uses described herein.

Suitable preparations of such vaccines include injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to  
25 injection, may also be prepared. The preparation may also be emulsified, or the polypeptides encapsulated in liposomes. The active immunogenic ingredients are often mixed with excipients which are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, buffered saline, dextrose, glycerol, ethanol, sterile isotonic aqueous buffer or the like and combinations  
30 thereof. In addition, if desired, the vaccine preparation may also include minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, and/or adjuvants which enhance the effectiveness of the vaccine.

Examples of adjuvants which may be effective, include, but are not limited to: aluminum hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-  
35 nor-muramyl-L-alanyl-D-isoglutamine, N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine.

The effectiveness of an adjuvant may be determined by measuring the induction of anti-idiotypic antibodies directed against the injected immunoglobulin formulated with the particular adjuvant.

The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, 5 sustained release formulation, or powder. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc.

Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water-free concentrate in a 10 hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is administered by injection, an ampoule of sterile diluent can be provided so that the ingredients may be mixed prior to administration.

In a specific embodiment, the lyophilized modified immunoglobulin of the invention is provided in a first container; a second container comprises diluent consisting of 15 an aqueous solution of 50% glycerin, 0.25% phenol, and an antiseptic (*e.g.*, 0.005% brilliant green).

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the vaccine formulations of the invention. Associated with such container(s) can be a notice in the form prescribed by a 20 governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may 25 for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Composition comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

30 The subject to which the vaccine is administered is preferably a mammal, most preferably a human, but can also be a non-human animal including but not limited to cows, horses, sheep, pigs, fowl (*e.g.*, chickens), goats, cats, dogs, hamsters, mice and rats.

Many methods may be used to introduce the vaccine formulations of the invention; these include but are not limited to oral, intracerebral, intradermal, intramuscular, 35 intraperitoneal, intravenous, subcutaneous, intranasal routes, and via scarification

(scratching through the top layers of skin, *e.g.*, using a bifurcated needle) or any other standard routes of immunization. In a specific embodiment, scarification is employed.

The precise dose of the modified immunoglobulin molecule to be employed in the formulation will also depend on the route of administration, and the nature of the patient, and should be decided according to the judgment of the practitioner and each patient's circumstances according to standard clinical techniques. An effective immunizing amount is that amount sufficient to produce an immune response to the modified immunoglobulin molecule in the host (*i.e.*, an anti-idiotypic reaction) to which the vaccine preparation is administered. Effective doses may also be extrapolated from dose-response curves derived from animal model test systems.

#### **5.4. METHOD OF PRODUCING THE MODIFIED IMMUNOGLOBULINS**

The modified immunoglobulins of the invention can be produced by any method known in the art for the synthesis of immunoglobulins, in particular, by chemical synthesis or by recombinant expression, and is preferably produced by recombinant expression techniques.

Recombinant expression of the modified immunoglobulin of the invention, or fragment, derivative or analog thereof, requires construction of a nucleic acid that encodes the modified immunoglobulin. If the nucleotide sequence of the modified immunoglobulin is known, a nucleic acid encoding the modified immunoglobulin may be assembled from chemically synthesized oligonucleotides (*e.g.*, as described in Kutmeier et al., 1994, *BioTechniques* 17:242), which, briefly, involves the synthesis of overlapping oligonucleotides containing portions of the sequence encoding the modified immunoglobulin, annealing and ligation of those oligonucleotides, and then amplification of the ligated oligonucleotides by PCR, *e.g.*, as exemplified in Section 6, *infra*.

Alternatively, the nucleic acid encoding the modified immunoglobulin may be generated from a nucleic acid encoding the immunoglobulin from which the modified immunoglobulin was derived. If a clone containing the nucleic acid encoding the particular immunoglobulin is not available, but the sequence of the immunoglobulin molecule is known, a nucleic acid encoding the immunoglobulin may be obtained from a suitable source (*e.g.*, an antibody cDNA library, or cDNA library generated from any tissue or cells expressing the immunoglobulin) by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by hybridization using an oligonucleotide probe specific for the particular gene sequence.

If an immunoglobulin molecule that specifically recognizes a particular antigen is not available (or a source for a cDNA library for cloning a nucleic acid encoding such an

immunoglobulin is not available), immunoglobulins specific for a particular antigen may be generated by any method known in the art, for example, by immunizing an animal, such as a rabbit, to generate polyclonal antibodies or, more preferably, by generating monoclonal antibodies, *e.g.*, as described by Kohler and Milstein (1975, *Nature* 256:495-497) or, as  
5 described by Kozbon et al. (1983, *Immunology Today* 4:72) or Cole et al. (1985 in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). Alternatively, a clone encoding at least the Fab portion of the immunoglobulin can be obtained by screening Fab expression libraries (*e.g.*, as described in Huse et al., 1989, *Science* 246:1275-1281) for clones of Fab fragments that bind the specific antigen or by screening  
10 antibody libraries (see, *e.g.*, Clackson et al., 1991, *Nature* 352:624; Hane et al., 1997 *Proc. Natl. Acad. Sci. USA* 94:4937).

Once a nucleic acid encoding at least the variable domain of the immunoglobulin molecule is obtained, it may be introduced into any available cloning vector, and may be introduced into a vector containing the nucleotide sequence encoding the constant region of  
15 the immunoglobulin molecule (see, *e.g.*, PCT Publication WO 86/05807; PCT Publication WO 89/01036; U.S. Patent No. 5,122,464; and Bebbington, 1991, *Methods in Enzymology* 2:136-145). Vectors containing the complete light or heavy chain for co-expression with the nucleic acid to allow the expression of a complete antibody molecule are also available, see *Id.* Then, the nucleic acid encoding the immunoglobulin can be modified to introduce  
20 the nucleotide substitutions or deletion necessary to substitute (or delete) the one or more variable region cysteine residues participating in an intrachain disulfide bond with an amino acid residue that does not contain a sulphydryl group, along with any other desired amino acid substitutions, deletions or insertions. Such modifications can be carried out by any method known in the art for the introduction of specific mutations or deletions in a  
25 nucleotide sequence, for example, but not limited to, chemical mutagenesis, *in vitro* site directed mutagenesis (Hutchinson et al., 1978, *J. Biol. Chem.* 253:6551), PCR based methods, etc.

In addition, techniques developed for the production of chimeric antibodies (Morrison et al., 1984, *Proc. Natl. Acad. Sci.* 81:851-855; Neuberger et al., 1984, *Nature*  
30 312:604-608; Takeda et al., 1985, *Nature* 314:452-454) by splicing genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can also be used. As described *supra*, a chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine monoclonal  
35 antibody and a constnat region derived from a human immunoglobulin, *e.g.*, humanized antibodies.

Alternatively, techniques described for the production of single chain antibodies (U.S. Patent 4,694,778; Bird, 1988, *Science* 242:423-42; Huston et al., 1988, *Proc. Natl. Acad. Sci. USA* 85:5879-5883; and Ward et al., 1989, *Nature* 334:544-54) can be adapted to produce single chain antibodies. Single chain antibodies are formed by linking the heavy  
 5 and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide. Techniques for the assembly of functional Fv fragments in *E. coli* may also be used (Skerra et al., 1988, *Science* 242:1038-1041).

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, such fragments include but are not limited to: the F(ab')<sub>2</sub>  
 10 fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the F(ab')<sub>2</sub> fragments.

Once a nucleic acid encoding the modified immunoglobulin molecule of the invention has been obtained, the vector for the production of the immunoglobulin molecule  
 15 may be produced by recombinant DNA technology using techniques well known in the art. The modified immunoglobulin molecule can then be recombinantly expressed and isolated by any method known in the art, for example, using the method described in Section 6, *supra*, (see also Bebbington, 1991, *Methods in Enzymology* 2:136-145). Briefly, COS cells, or any other appropriate cultured cells, can be transiently or non-transiently  
 20 transfected with the expression vector encoding the modified immunoglobulin, cultured for an appropriate period of time to permit immunoglobulin expression, and then the supernatant can be harvested from the COS cells, which supernatant contains the secreted, expressed modified immunoglobulin.

Methods which are well known to those skilled in the art can be used to construct  
 25 expression vectors containing the immunoglobulin molecule coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. See, for example, the techniques described in Sambrook et al. (1990, *Molecular Cloning, A Laboratory Manual*, 2d Ed., Cold Spring Harbor Laboratory, Cold  
 30 Spring Harbor, NY) and Ausubel et al. (eds., 1998, *Current Protocols in Molecular Biology*, John Wiley & Sons, NY).

The expression vector is transferred to a host cell by conventional techniques and the transfected cells are then cultured by conventional techniques to produce the immunoglobulin of the invention.

35 The host cells used to express the recombinant antibody of the invention may be either bacterial cells such as *Escherichia coli*, or, preferably, eukaryotic cells, especially for

the expression of whole recombinant immunoglobulin molecules. In particular, mammalian cells such as Chinese hamster ovary cells (CHO), in conjunction with a vector such as the major intermediate early gene promoter element from human cytomegalovirus is an effective expression system for immunoglobulins (Foecking et al., 198, *Gene* 45:101; 5 Cockett et al., 1990, *Bio/Technology* 8:2).

A variety of host-expression vector systems may be utilized to express the modified immunoglobulin molecules of the invention. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells which may, when transformed or transfected with the 10 appropriate nucleotide coding sequences, express the immunoglobulin molecule of the invention in situ. These include but are not limited to microorganisms such as bacteria (*e.g.*, *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing immunoglobulin coding sequences; yeast (*e.g.*, *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors 15 containing immunoglobulin coding sequences; insect cell systems infected with recombinant virus expression vectors (*e.g.*, baculovirus) containing the immunoglobulin coding sequences; plant cell systems infected with recombinant virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (*e.g.*, Ti plasmid) containing immunoglobulin 20 coding sequences; or mammalian cell systems (*e.g.*, COS, CHO, BHK, 293, 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (*e.g.*, metallothionein promoter) or from mammalian viruses (*e.g.*, the adenovirus late promoter; the vaccinia virus 7.5K promoter).

In bacterial systems, a number of expression vectors may be advantageously 25 selected depending upon the use intended for the immunoglobulin molecule being expressed. For example, when a large quantity of such a protein is to be produced, for the generation of pharmaceutical compositions of an immunoglobulin molecule, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector 30 pUR278 (Ruther et al., 1983, *EMBO J.* 2:1791), in which the immunoglobulin coding sequence may be ligated individually into the vector in frame with the *lac Z* coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, 1985, *Nucleic Acids Res.* 13:3101-3109; Van Heeke & Schuster, 1989, *J. Biol. Chem.* 24:5503-5509); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins 35 with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption and binding to a matrix glutathione-

agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

In an insect system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The immunoglobulin coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the immunoglobulin coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by *in vitro* or *in vivo* recombination. Insertion in a non-essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing the immunoglobulin molecule in infected hosts (e.g., see Logan & Shenk, 1984, *Proc. Natl. Acad. Sci. USA* 81:355-359). Specific initiation signals may also be required for efficient translation of inserted immunoglobulin coding sequences. These signals include the ATG initiation codon and adjacent sequences. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner et al., 1987, *Methods in Enzymol.* 153:51-544).

In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include but are not limited to CHO, VERO, BHK, HeLa, COS, MDCK, 293, 3T3, WI38.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express the immunoglobulin molecule may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the immunoglobulin molecule. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that interact directly or indirectly with the immunoglobulin molecule.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler et al., 1977, *Cell* 11:223), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, 1972, *Proc. Natl. Acad. Sci. USA* 48:202), and adenine phosphoribosyltransferase (Lowy et al., 1980, *Cell* 22:817) genes can be employed in tk<sup>-</sup>, hgprt<sup>-</sup> or aprt<sup>-</sup> cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler et al., 1980, *Natl. Acad. Sci. USA* 77:357; O'Hare et al., 1981, *Proc. Natl. Acad. Sci. USA* 78:1527); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, 1981, *Proc. Natl. Acad. Sci. USA* 78:2072); neo, which confers resistance to the aminoglycoside G-418 (*Clinical Pharmacy* 12:488-505; Wu and Wu, 1991, *Biotherapy* 3:87-95; Tolstoshev, 1993, *Ann. Rev. Pharmacol. Toxicol.* 32:573-596; Mulligan, 1993, *Science* 260:926-932; and Morgan and Anderson, 1993, *Ann. Rev. Biochem.* 62:191-217; May, 1993, *TIBTECH* 11(5):155-215). Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al. (eds.), 1993, *Current Protocols in Molecular Biology*, John Wiley & Sons, NY; Kriegler, 1990, *Gene Transfer and Expression, A Laboratory Manual*, Stockton Press, NY; and in Chapters 12 and 13, Dracopoli et al. (eds), 1994, *Current Protocols in Human Genetics*, John Wiley & Sons, NY.; Colberre-Garapin et al., 1981, *J. Mol. Biol.* 150:1.

Alternatively, any fusion protein may be readily purified by utilizing an antibody specific for the fusion protein being expressed. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., 1991, *Proc. Natl. Acad. Sci. USA* 88:8972-897). In

this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an amino-terminal tag consisting of six histidine residues. The tag serves as a matrix binding domain for the fusion protein. Extracts from cells infected with recombinant vaccinia virus are loaded onto  
 5  $\text{Ni}^{2+}$ -nitriloacetic acid-agarose columns and histidine-tagged proteins are selectively eluted with imidazole-containing buffers.

The expression levels of the immunoglobulin molecule can be increased by vector amplification (for a review, see Bebbington and Hentschel, *the Use of Vectors Based on Gene Amplification for the Expression of Cloned Genes in Mammalian Cells in DNA*  
 10 *Cloning*, Vol.3. (Academic Press, New York, 1987)). When a marker in the vector system expressing immunoglobulin is amplifiable, increase in the level of inhibitor present in culture of host cell will increase the number of copies of the marker gene. Since the amplified region is associated with the immunoglobulin gene, production of the immunoglobulin will also increase (Crouse et al., 1983, *Mol. Cell. Biol.* 3:257).

15 The host cell may be co-transfected with two expression vectors of the invention, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors may contain identical selectable markers which enable equal expression of heavy and light chain polypeptides. Alternatively, a single vector may be used which encodes both heavy and light chain polypeptides. In such  
 20 situations, the light chain should be placed before the heavy chain to avoid an excess of toxic free heavy chain (Proudfoot, 1986, *Nature* 322:52; Kohler, 1980, *Proc. Natl. Acad. Sci. USA* 77:2197). The coding sequences for the heavy and light chains may comprise cDNA or genomic DNA.

Once the modified immunoglobulin molecule of the invention has been  
 25 recombinantly expressed, it may be purified by any method known in the art for purification of an immunoglobulin molecule, for example, by chromatography (e.g., ion exchange, affinity, particularly by affinity for the specific antigen after Protein A, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins.

30

### **5.5. DEMONSTRATION OF THERAPEUTIC UTILITY**

The modified antibodies of the invention can be screened or assayed in a variety of ways for efficacy in treating or preventing a particular disease .

First, the immunopotency of a vaccine formulation containing the modified antibody  
 35 of the invention can be determined by monitoring the anti-idiotypic response of test animals following immunization with the vaccine. Generation of a humoral response may be taken

as an indication of a generalized immune response, other components of which, particularly cell-mediated immunity, may also be important. Test animals may include mice, rabbits, chimpanzees and eventually human subjects. A vaccine made in this invention can be made to infect chimpanzees experimentally. However, since chimpanzees are a protected species,  
 5 the antibody response to a vaccine of the invention can first be studied in a number of smaller, less expensive animals, with the goal of finding one or two best candidate immunoglobulin molecules or best combinations of immunoglobulin molecules to use in chimpanzee efficacy studies.

The immune response of the test subjects can be analyzed by various approaches  
 10 such as the reactivity of the resultant immune serum to antibodies, as assayed by known techniques, *e.g.*, enzyme linked immunosorbent assay (ELISA), immunoblots, radioimmunoprecipitations, etc.; or protection from infection and/or attenuation of disease symptoms in immunized hosts.

As one example of suitable animal testing, the vaccine composition of the invention  
 15 may be tested in rabbits for the ability to induce an anti-idiotypic response to the modified immunoglobulin molecule. For example, male specific-pathogen-free (SPF) young adult New Zealand White rabbits may be used. The test group of rabbits each receives an effective amount of the vaccine. A control group of rabbits receives an injection in 1 mM Tris-HCl pH 9.0 of the vaccine containing a naturally occurring antibody. Blood samples  
 20 may be drawn from the rabbits every one or two weeks, and serum analyzed for anti-idiotypic antibodies to the modified immunoglobulin molecule and anti-anti-idiotypic antibodies specific for the antigen against which the modified antibody was directed using, *e.g.*, a radioimmunoassay (Abbott Laboratories). The presence of anti-idiotypic antibodies may be assayed using an ELISA. Because rabbits may give a variable response due to their  
 25 outbred nature, it may also be useful to test the vaccines in mice.

In addition, a modified antibody of the invention may be tested by first administering the modified antibody to a test subject, either animal or human, and then isolating the anti-anti-idiotypic antibodies (*i.e.*, the Ab3 antibodies) generated as part of the anti-idiotypic response to the injected modified antibody. The isolated Ab3 may then be  
 30 tested for the ability to bind the particular antigen (*e.g.*, a tumor antigen, antigen of an infectious disease agent by any immunoassays known in the art, for example, but not limited to, radioimmunoassays, ELISA, "sandwich" immunoassay, gel diffusion precipitin reactions, immunodiffusion assays, western blots, precipitation reactions, agglutination assays, complement fixation assays, immunofluorescence assays, protein A assays,  
 35 immunoelectrophoresis assays, etc.

Additionally, the modified antibodies of the invention may also be tested directly *in vivo*. The strength of the immune response *in vivo* to the modified immunoglobulin may be determined by any method known in the art, for example, but not limited to, delayed hypersensitivity skin tests and assays of the activity of cytolytic T-lymphocytes *in vitro*.

5 Delayed hypersensitivity skin tests are of great value in the testing of the overall immunocompetence and cellular immunity to an antigen. Proper technique of skin testing requires that the antigens be stored sterile at 4°C, protected from light and reconstituted shortly before use. A 25- or 27-gauge needle ensures intradermal, rather than subcutaneous, administration of antigen. Twenty-four and 48 hours after intradermal administration of the  
10 antigen, the largest dimensions of both erythema and induration are measured with a ruler. Hypoactivity to any given antigen or group of antigens is confirmed by testing with higher concentrations of antigen or, in ambiguous circumstances, by a repeat test with an intermediate test.

To test the activity of cytolytic T-lymphocytes, T-lymphocytes isolated from the  
15 immunized subject, *e.g.*, by the Ficoll-Hypaque centrifugation gradient technique, are restimulated with cells bearing the antigen against which the modified antibody was directed in 3 ml RPMI medium containing 10% fetal calf serum. In some experiments, 33% secondary mixed lymphocyte culture supernatant or IL-2 is included in the culture medium as a source of T cell growth factors. In order to measure the primary response of cytolytic  
20 T-lymphocytes after immunization, the isolated T cells are cultured with or without the cells bearing the antigen. After six days, the cultures are tested for cytotoxicity in a 4 hour <sup>51</sup>Cr-release assay. The spontaneous <sup>51</sup>Cr-release of the targets should reach a level less than 20% if immunization was effective (Heike et al., *J. Immunotherapy* 15:15-174).

The efficacy of the modified antibody as a contraceptive can also be tested by any  
25 method known for tested contraceptive methods. For example, a vaccine composition containing a modified antibody of the invention specific for an antigen of a protein or cell involved in reproductive function. First, the level of the particular antigen in the subject can be measured by any method known in the art where a reduction in the level of the antigen compared to the level prior to administration of the modified antibody (accounting for  
30 normal, cyclical changes of the level of the particular antigen) indicates that the modified antibody may be effective. The modified antibody must then be administered to a population of child bearing age (and having partners of childbearing age) and the percentage of females that conceive over a suitable period of time is determined. If the number of females that conceive is significantly lower than those in a control population, *e.g.*, those  
35 administered a placebo or not using a contraceptive method, indicates that the modified antibody is effective as a contraceptive.

Additionally, the efficacy of the contraceptive vaccine may be assayed by administering the vaccine to a subject or animal model, allowing an appropriate amount of time for the production of anti-idiotypic antibodies, and then testing serum taken from the subject or animal for the ability to bind the particular antigen (indicating that an anti-  
 5 idiotypic reaction has occurred) and/or testing whether the serum can block fertilization in vitro, which can be tested by any method known in the art, for example as described in Brannen-Brock et al., 1985, Arch. Androl. 15:15-19. .

## 6. EXAMPLE: ANTI-IDIOTYPIC VACCINE INDUCER FOR COLON 10 CANCER

This example describes the construction of a modified antibody derived from the monoclonal antibody MAb31.1 (hybridoma secreting Mab31.1 is available from the American Type Tissue Collection as accession No. HB12314). Mab31.1 recognizes an  
 15 antigen expressed by human colon carcinomas. The modified antibody of the invention, based on Mab31.1, was engineered to have variable region cysteine residues of both the heavy and light chain variable regions substituted with alanine. Therefore, the resulting modified antibody, was missing intrachain disulfide bonds in either the heavy and light chain variable regions.

20

### 6.1. CONSTRUCTION OF A MODIFIED ANTIBODY

The strategy for construction of the modified antibody was to construct two engineered genes that encoded the heavy and light chain variable regions wherein specific cysteine residues, known to be important in intra-chain disulfide bonding , were altered to  
 25 alanine. Alanine residues were substituted for the cysteine residues at positions 22 and 92 of the heavy chain variable region of the antibody derived from Mab31.1 or at positions 23 and 88 of the Mab31.1 light chain variable region of the antibody derived from Mab31.1. In order to construct these engineered genes, groups of oligonucleotides were assembled (as discussed below) and inserted into an appropriate vector providing constant regions.

30 In order to construct variable region genes encoding CDRs lacking intrachain disulfide bonds, the following strategy was performed.

First, single strand oligonucleotides were annealed to create cohesive double stranded DNA fragments (as diagramed in Figure 8, Step 1). Specifically, oligonucleotides of about 80 bases in length corresponding to the sequences of interest with 20 base  
 35 overlapping regions were synthesized using automated techniques of GenoSys Biotech Inc. The specific sequences of each of these oligonucleotides. The specific sequences of these

oligonucleotides are presented in Figures 16A and 16B. Figure 16A list the group of ten oligos used in engineering a heavy chain variable region gene called 2CAVHCOL1. 2CAVHCOL1 lacked 2 cysteine residues as compared to the consensus heavy chain variable gene. Figure 16B lists the group of 12 oligos used in the engineering of the light chain variable region gene called 2CAVLCOL1. 2CAVLCOL1 lacked two cysteine residues as compared to the consensus light chain variable region gene. In order to combine the oligos into the desired gene, groups of 10 or 12 oligos were combined as described below and as presented in Figure 8, where the identities of oligos 1 to 10 indicated in Figure 8 are provided in Table 5. Prior to combining, each oligonucleotide was 5' phosphorylated as follows: 25µl of each oligo was incubated for 1 hour in the presence of T4 polynucleotide kinase and 50mM ATP at 37°C. The reactions were stopped by heating for 5 minutes at 70°C followed by ethanol precipitation. Once phosphorylated, complementary oligonucleotides (oligo 1 + oligo 10, oligo 2 + oligo 9, oligo 3 + oligo 8, oligo 4 + oligo 7, oligo 5 + oligo 6), as shown in Figure 8, were then mixed in sterile microcentrifuge tubes and annealed by heating the tube in a water bath at 65°C for 5 minutes followed by cooling at room temperature for 30 minutes. Annealing resulted in short double strand DNA fragments with cohesive ends.

Next, the cohesive double stand DNA fragments were ligated into longer strands (Figure 8, Steps 2-4), until the engineered variable region gene was assembled. Specifically, cohesive double strand DNA fragments were ligated in the presence of T4 DNA ligase and 10mM ATP for 2 hours in a water bath maintained at 16°C. Annealed oligo 1/10 was mixed with annealed oligo 2/9, and annealed oligo 3/8 was mixed with annealed oligo 4/7. The resulting oligos were labeled oligo 1/10/2/9 and oligo 3/8/4/7. Next, oligo 3/8/4/7 was ligated to oligo 5/6. The resulting oligo 3/8/4/7/5/6 was then ligated to oligo 1/10/2/9 resulted in a full length variable region gene.

Alternatively, when groups of 12 oligos were used, the order of addition was: 1+12 = 1/12, 2+11=2/11, 3+10=3/10, 4+9=4/9, 5+8=5/8, 6+7=6/7, 1/12+2/11=1/12/2/11, 3/10+4/9=3/10/4/9, 5/8+6/7=5/8/6/7, 1/12/2/11+3/10/4/9 = 1/12/2/11/3/10/4/9, 1/12/2/11/3/10/4/9+5/8/6/7= full length variable region gene. The names of oligonucleotides used in construction of the engineered genes are listed in Table 5. The modified heavy chain variable region gene was denoted as 2CAVHCOL1. The modified light chain variable region gene was denoted as 2CAVLCOL1.

The resulting modified variable region genes were then purified by gel electrophoresis. To remove unligated excess of oligos and other incomplete DNA fragments, ligated product was run on 1% low melting agarose gel at constant 110 V for 2 hours. The major band containing full length DNA product was cut out and placed in a

sterile 1.5 ml centrifuge tube. To release the DNA from the agarose, the gel slice was digested with *f3*-Agrase I at 40°C for 3 hours. The DNA was recovered by precipitation with 0.3 M NaOAc and isopropanol at -20°C for 1 hour followed by centrifugation at 12,000 rpm for 15 minutes. The purified DNA pellet was resuspended in 50 µl of TE buffer, pH 8.0. The engineered variable region gene was then amplified by PCR. Specifically, 100 ng of the engineered variable region gene was mixed with 25mM dNTPs, 200 ng of primers and 5 U of high fidelity thermostable Pfu DNA polymerase in buffer. Resulting PCR product was analyzed on 1% agarose gel.

Each purified DNA corresponding to the engineered variable region gene was subsequently inserted into the pUC19 bacterial vector. pUC19, is a 2686 base pair, a high copy number *E. coli* plasmid vector containing a 54 base pair polylinker cloning site in *lacZ* and an Amp selection marker. In order to prepare the vector for insertion of the engineered variable region gene, 10µg of pUC19 was linearized with *Hinc II* (50 U) for 3 hours at 37°C resulting in a vector with blunt end sequence 5' GTC. To prevent self re-ligation, linear vector DNA was dephosphorylated with 25 U of calf intestine alkaline phosphatase (CIP) for 1 hour at 37°C. In order to insert the engineered variable region gene into the pUC19 vector, approximately 0.5 µg of dephosphorylated linear vector DNA was mixed with 3 µg of phosphorylated variable region gene in the presence of T4 DNA ligase (1000 U), and incubated at 16°C for 12 hours.

The bacterial vector containing the engineered variable region gene was then used to transform bacterial cells. Specifically, freshly prepared competent DH5-α cells, 50 µl, were mixed with 1 µg of pUC19 containing the engineered variable region gene and transferred to an electroporation cuvette (0.2 cm gap; Bio-Rad). Each cuvette was pulsed at 2.5 kV/200 ohm/25 µF in an electroporator (Bio-Rad Gene Pulser). Immediately thereafter, 1 ml of SOC media was added to each cuvette and cells were allowed to recover for 1 hour at 37°C in centrifuge tubes. An aliquot of cells from each transformation was removed, diluted 1:100, then 100 µl plated onto LB plates containing ampicillin (Amp 40 µg/ml). The plates were incubated at 37°C overnight due to the presence of the Amp marker. Only transformants containing pUC19 vector grew on LB/Amp plates.

A single transformant colony was picked and grown overnight in a 3 ml LB/Amp sterile glass tube with constant shaking at 37°C. The plasmid DNA was isolated using Easy Prep columns (Pharmacia Biotech.) and suspended in 100 µl of TE buffer, pH 7.5. To confirm the presence of gene insert in pUC19, 25 µl of plasmid DNA from each colony was digested with a restriction endonuclease for 1 hour at 37°C, and was analyzed on a 1% agarose gel. By this method plasmid DNA containing gene insert was resistant to enzyme cleavage due to loss of restriction site ( 5'..GTCGAC.. 3') and migrated as closed circular

(CC) DNA, while those plasmids without insert were cleaved and migrated as linear (L) double strand DNA fragment on gel.

In order to confirm correct gene sequences of the engineered variable region genes and to eliminate the possibility of unwanted mutations generated during the construction procedure, DNA sequencing was performed using M13/pUC reverse primer (5'AACAGCTATGACCATG 3') for the clones as well as PCR gene products using 5' end 20 base primer ( 5' GAATT CATGGCTTG GGTGTG 3') on automated ABI 377 DNA Sequencer. All clones were confirmed to contain correct sequences.

10 **Table 5. Construction of gene encoding modified antibodies containing CDRs from Mab 31.1**

	Oligo1	Oligo 2	Oligo 3	Oligo 4	Oligo 5	Oligo	Oligo 7	Oligo 8	Oligo 9	Oligo10
2CAVHC	VHC1	VHC2	VHC3	VHC4	VHC5	VHC	VHC7	VHC8	VHC9	VHC10
OLI										
2CAVLC	VLC1	VLC2	VLC3	VLC4	VLC5	VLC	VLC7	VLC8	VLC9	VLC10
OLI										

### 6.3. INSERTION OF THE ENGINEERED VARIABLE REGION GENE INTO A MAMMALIAN EXPRESSION VECTOR

A complete antibody light chain has both a variable region and a constant region. A complete antibody heavy chain contains a variable region, a constant region, and a hinge region. A modified variable region genes 2CAVHCOL1 or 2CAVLCOL1 were inserted into vectors containing appropriate constant regions. Engineered variable region genes lacking cysteine residues in the light chain, were inserted into the pMRRO10.1 vector Figure 6A. The pMRRO10.1 vector contained a human kappa light chain constant region. Insertion of the engineered light chain variable region into this vector gave a complete light chain sequence. Alternatively, the engineered variable region gene lacking cysteine residues in the heavy chain, were inserted into the pGAMMA1 vector Figure 6B. The pGAMMA1 vector contained human and IgG1 constant region and hinge region sequences. Insertion of the engineered heavy chain variable region gene into this vector gave a complete heavy chain sequence.

In order to engineer a mammalian vector comprising both heavy chain and light chain genes, the complete light chain sequence and complete heavy chain sequence were inserted into mammalian expression vector pNEPuDGV as shown in Figure 6C (Bebbington, C.R., 1991, In METHODS: A Companion to Methods in Enzymology, vol. 2, pp. 136-145). The resulting vector encoding both light chain and the heavy chain of the modified antibody.

#### 6.4. EXPRESSION OF SYNTHETIC MODIFIED ANTIBODIES IN MAMMALIAN CELLS

To examine the production of assembled antibodies the mammalian expression vector was transfected into COS cells. COS cells (an African green monkey kidney cell line, CV-1, transformed with an origin-defective SV40 virus) were used for short-term transient expression of the synthetic antibodies because of their capacity to replicate circular plasmids containing an SV40 origin of replication to very high copy number. The antibody expression vector was transferred to COS7 cells (obtained from the American Type Culture Collection). The transfected cells were grown in Dulbecco's modified Eagle's Medium and transfected with the expression vectors using calcium precipitation (Sullivan et al., *FEBS Lett.* 285:120-123, 1991). The transfected cells were cultured for 72 hours after which supernatants were collected. Supernatants from transfected COS cells were assayed using ELISA method for assembled IgG. ELISA involves capture of the samples and standards onto a 96-well plate coated with an anti-human IgG Fc. Bound assembled IgG was detected with an anti-human Kappa chain linked to horse radish peroxidase (HRP) and the substrate tetramethylbenzidine (TMB). Color development was proportional to the amount of assembled antibody present in the sample.

#### 6.5. MODIFIED ANTIBODY IMMUNOSPECIFICALLY BINDS TO HUMAN COLON CARCINOMA CELLS AND ANTIGENS PRODUCED BY THESE CELLS

The modified antibody was expressed and isolated as indicated in Section 6.4, *supra*. The binding capacity and specificity were then assayed using LS-174T cells WiDR cells (a human colon cancer cell line) and an antigen derived from these cells.

In order to examine the binding potency as well as specificity of MA31.1 binding, a dot blot analysis was performed (see Figure 9). Membrane preparations from LS-174T cells was applied to a nitrocellulose membrane using a Bio-Blot apparatus (Bio-Rad). The wells were blocked for non-specific binding using skim milk. Biotinylated antibody derived from Mab31.1 was incubated in all wells. Unlabelled antibody at concentrations of 0.003 to 20 nM was then applied to the nitrocellulose membrane and allowed to incubate. Unbound antibody was removed from the membrane by washing and a second antibody, alkaline phosphatase labeled antihuman IgG, was added. Finally, an alkaline phosphatase substrate was added which generated a dark purple precipitate, indicating the presence of bound labeled antibody. Figure 9 provides the results of the dot blot analysis. The figure demonstrated that the labeled antibody bound to the LS-174 T cells. Additionally, the unlabeled antibody competed with biotinylated antibody binding, indicating specificity of binding of the antibody derived from Mab31.1 to tumor cell antigens.

## 6.6. ANTI-IDIOTYPE RESPONSE

The effect on binding of modified antibody to LS-174T cells was examined in a competition binding assay. LS-174T cells are human colon carcinoma cells which express antigen recognized by the Mab31.1 antibody. Peptides containing the sequence of one of the CDRs of the Mab31.1 antibody were generated. These peptides, the modified antibody and the control antibody derived from Mab31.1 were administered to mice in order to generate antisera against the CDR regions of Mab31.1 and the antibodies. Blood samples from mice were drawn two weeks and four weeks following injection. Antisera from the immunized mice were used in binding competition assays presented in Figures 10A and B.

Antisera and biotinylated antibodies were assayed for their ability to bind LS-174T cells. As demonstrated in Figure 10A and B, antisera raised to the CDR3 and CDR4 peptides dramatically competed for control antibody (antibody derived from Mab31.1) binding to LS-174T cells. Additionally, antisera raised against CDR1 and CDR2 also significantly competed for control antibody binding to LS-174T cells. Additionally, antisera from mice injected with the 2CAVHCOL1 and 2CAVLCOL1 antibodies (*i.e.*, the modified antibodies having the cysteine to alanine change in the variable region) competed for binding with the biotinylated antibody derived from Mab31.1 better than antiserum from mice injected with the antibody derived from Mab31.1 (Figure 10B). This result indicates that administration of the antibodies having the cysteine to alanine change in the variable region elicit an anti-idiotypic antibodies that recognize the colon carcinoma cell antigen better than antibodies with variable region intra-chain disulfide bonds.

**Table 6.      Biotin-Labeled Peptides Derived from CDR Sequences of Mab 31.1**

Peptide ID	Sequence
COL311 L1	biotin-N-Thr-Ala-Lys-Ala-Ser-Gln-Ser-Val-Ser-Asn-Asp-Val-Ala
COL311 L2	biotin-N-Ile-Tyr-Tyr-Ala-Ser-Asn-Arg-Tyr-Thr
COL311 L3	biotin-N-Phe-Ala-Gln-Gln-Asp-Tyr-Ser-Ser-Pro-Leu-Thr
COL311 H1	biotin-N-Phe-Thr-Asn-Tyr-Gly-Met-Asn
COL311 H2	biotin-N-Ala-Gly-Trp-Ile-Asn-Thr-Tyr-Thr-Gly-Glu-Pro-Thr-Tyr-Ala-Asp-Asp-Phe-Lys-Gly
COL311 H3	biotin-N-Ala-Arg-Ala-Tyr-Tyr-Gly-Lys-Tyr-Phe-Asp-Tyr

## 7. EXAMPLE: SPERM ANTIGEN VACCINES

The example herein describes the construction of defined epitopes that replace the complementarity determining regions (CDR) of an antibody. Specifically, the

epitopes are derived from sperm antigens SP-10, LDH-C<sub>4</sub> or MSA-63. These constructs express an antibody, which, when injected into an appropriate host, induces an immune reaction that precipitates the formation of anti-idiotypic antibodies that are active against the sperm antigens.

- 5           The strategy for producing the antibody containing a sperm cell epitope is outlined as follows: (1) a CDR is engineered to contain a nucleotide sequence encoding one or more epitopes from a sperm specific protein, (2) the engineered CDR is then cloned into a mammalian expression vector containing the appropriate heavy or light chain constant regions, (3) the vector is transfected into a cell that supports expression, proper folding and
- 10       modification of functional antibodies, (4) the antibody is harvested from the supernatant and is confirmed for the epitope expression by standard assays (e.g. ELISA, western blot, etc.), and (5) the antibody is used as an immunogen in an appropriate host to generate anti-sperm antibodies, thereby inducing long lasting infertility.

#### 15           7.1.    CONSTRUCTION OF THE SPERM ANTIGEN VACCINE

The following describes the construction of a modified variable region gene containing at least one CDR that contains a sperm antigen epitope, *i.e.*, SP-10 or LDH-C<sub>4</sub> epitope and/or an MSA-63 epitope.

- First, an epitope is chosen and defined so that oligonucleotides may be
- 20       synthesized. In the following example, an SP-10 epitope from the sperm antigen SP-10 is used. SP-10 is a suitable epitope because it is expressed exclusively in sperm cells. It is also expressed on the surface of the membrane of the acrosome, thus, it is accessible to therapeutic antibodies. Other antibodies are produced that contain portions of the LDH-C<sub>4</sub> and MSA-63 antigens.

- 25           The nucleotide and protein sequences of the SP-10 epitope are:

GAA TTC CAG CCT TCA GGT GAA CAT GGC TCC GGT GAA CAG CCT TCT GGT  
GAG CAG GCC TCG GGT GAA CAG CCT TCA GGT GAG CAC GCT TCA GGG GAA  
CAG GCT TCA GGT GCA CCA ATT TCA AGC ACA TCT ACA GGC ACA ATA TTA  
AAT TGC TAC ACA TGT GCT TAT ATG AAT GAT CAA GGA AAA TGT CTT CGT  
GGA GAG GGA ACC TGC ATC ACT CAG AAT TC;

- 30       Gln Pro Ser Gly Glu His Gly Glu Gln Pro Ser Gly Glu Gln Ala Ser Gly Glu Gln Pro Ser gly  
Glu His Ala Ser Gly Glu Gln Ala Ser Gly Ala Gln Ile Ser Ser Thr Ser Thr Gly Thr Ile Leu  
Asn Cys Tyr Thr Cys Ala Tyr Met Asn Asp Gln Gly Lys Cys Leu Arg Gly Glu Gly Thr  
Cys Ile Thr Gln Asn.

- The replacement of an antibody's CDR with another epitope is made easier by the fact that the variable region sequence of antibodies are relatively short, and are
- 35       known. One is then able to synthetically generate a series of complementary oligonucleotides that, when annealed and ligated, reconstruct the entire coding region of

variable region portion of the gene. In this manner, the CDR is replaced with sequences of the epitope of interest, in this example, SP-10. The following is a list of the sequences of the oligonucleotides designed for cloning SP-10 epitopes into the CDR:

- 5 **Oligo SP 1:**  
GAA TTC CAG CCT TCA GGT GAA CAT GGC TCC GGT GAA CAG CCT TCT GGT  
GAG CAG GCC TCG GGT GAA CAG CCT TAG,  
**Oligo SP 2:**  
GTG AGC ACG CTT CAG GGG AAC AGC CTT CAG GTG CAC CAA TTT CAA GCA  
CAT CTA CAG GCA CAA TAT TAA ATT GCT,  
**Oligo SP 3:**  
10 ACA CAT GTG CTT ATA TGA ATG ATC AAG GAA AAT GTC TTC GTG GAG AGG  
GAA CCT GCA TCA CTC AGA ATT C,  
**Oligo SP 3a(3Cys->Ala):**  
ACA CAG CAG CTT ATA TGA ATG ATC AAG GAA AAG CAC TTC GTG GAG AGG  
GAA CCG CAA TCA CTC AGA ATT C,  
**Oligo SP 4:**  
GAA TTC TGA GTG ATG CAG GTT CCC TCT CCA CGA AGA CAT TTT CCT TGA  
TCA TTC ATA TAA GCA CAT GTG TAG CAA TTT A,  
**Oligo SP 4a (3Cys->Ala):**  
15 GAA TTC TGA GTG ATT GCG GTT CCC TCT CCA CGA AGT GCT TTT TGA TGA  
TCA TTC ATA TAA GCT GCT GTG TAG CAA TTT A,  
**Oligo SP 5:**  
ATA TTG TGC CTG TAG ATG TGC TTG AAA TTG GTG CAC CTG AAG CCT GTT  
CCC CTG AAG CGT GCT CAC CTG AAG GCT,  
**Oligo SP 6:**  
20 GTT CTC CCG AGG CCT GCT CAC CAG AAG GCT GTT CAC CGG AGC CAT GTT  
CAC CTG AAG GCT GGA ATT C.

Antibodies containing portions of the MSA-63 antigen are also described.

To identify the optimal portion of the antigen to be introduced into the antibody, oligonucleotides encoding different portions of the antigen are synthesized.

- 25 Practically, the first two amino acid codons of the sperm cell specific epitope, MSA-63, an oligonucleotide encoding residues 143 and 144 (i.e. GTC GGC, *infra*), is cloned into the immunoglobulin CDR, using the methods described *infra*. The MSA-63 DNA sequence encoding the epitope:

- 30 GTC GGC AGC CTC CGA AGC AGC CCG CTC CAG AGC CCG CTG CTC CGA CCG  
CTC GTC CAG AGC AGC CTC TGC TTG CTG TTC CTC TTG CTG CGA TAC AGC  
TGC GGC GAC GGC AGC TGC AGC CGA CGA TAC TGC GAC TTG ACG GTG TGC  
CGG CGA ATG TAC TTG CTG CTG CGA TTC ACG GAC CCG CCG CTC CCG CAG  
ACG TGC TGC GTC TTG AGC

The MSA-63 protein sequence epitope encoded by the nucleic acid sequence above, which starts at amino acid 143 and ends at 233.

- 35 Gln Pro Ser Glu Ala Ser Ser Gly Glu Val Ser Gly Asp Glu Ala Gly Glu Gln Val Ser Ser  
Glu Thr Asn Asp Lys Glu Asn Asp Ala Met Ser Thr Pro Leu Pro Ser Thr Ser Ala Ala Ile



Antibodies in which a portion of the MSA-63 antigen has been inserted into CDR1, *i.e.*, where residues Lys24 through Ala34 of the consensus contraceptive light chain, the sequence of which is in Figure 15, are replaced with the sequence Gln-Pro-Ser-Glu-Ala-Ser-Ser-Gly-Glu-Val-Ser-Gly-Asp-Glu-Ala-Gly-Glu. The antibody, MSA1, can be

5 constructed using the oligonucleotides provided in Figure 11 in the scheme provided in Figure 8 and described below, where the identities of oligonucleotides 1-12 are indicated in Table 7. The antibody MSA1VAC can also be constructed using the oligos of Figure 11 by the scheme of Figure 8, as indicated in Table 7. MSA1VAC is the same as MSA1 except that the cysteine at position 23 of the light chain variable region has been replaced with

10 alanine. These light chains can be expressed with the heavy chain consensus sequence CONVH1, the sequence of which is provided in Figure 7B, and the construction of which can be accomplished with the oligonucleotides as indicated in Table 4. These single stranded oligonucleotides sequences are annealed to create cohesive double stranded DNA fragments suitable for ligation as diagramed in Figure 8, along with oligonucleotides

15 encoding the remainder of the consensus variable region, to construct the variable region gene. For the MSA-63 containing variable regions MSA1 and MSA1VAC the oligonucleotides corresponding to oligonucleotides 1 to 10, or 1 to 12, of Figure 8 are provided in Table 7, and the sequences of these oligonucleotides are provided in Figure 11. Specifically, oligonucleotides of about 70 bases in length corresponding to the sequences of

20 interest with 20 base overlapping regions are synthesized (GenoSys Biotech Inc.). Each oligonucleotide is 5' phosphorylated as follows: 25 $\mu$ l of each oligo is incubated for one hour in the presence of T<sub>4</sub> polynucleotide kinase and 50 mM ATP in appropriate buffer at 37°C. The enzyme is heat killed and the reaction stopped by heating for ten minutes at 70°C followed by ethanol precipitation with sodium acetate. The oligos are then resuspended in

25 TE buffer (10 mM Tris, pH 8.0, 1 mM EDTA).

Complementary oligonucleotides (oligo 1 + oligo 10, oligo 2 + oligo 9, oligo 3 + oligo 8, oligo 4 + oligo 7, and oligo 5 + oligo 6) were then mixed in a sterile microcentrifuge tube and annealed by heating the tube in a water bath at 65°C for 5 minutes followed by cooling at room temperature for 30 minutes. Annealing results in double

30 stranded DNA with cohesive ends. The cohesive double stranded DNA fragments are ligated into longer strands (Figure 8, Steps 2-4), until the engineered variable region gene was assembled. Specifically, cohesive double stranded DNA fragments are ligated in the presence of T<sub>4</sub> DNA ligase, ligase buffer and 10 mM ATP for two hours in a water bath maintained at 16°C. Annealed oligo 1/10 is mixed with annealed oligo 2/9, and annealed

35 oligo 3/8 is mixed with annealed oligo 4/7. The resulting oligos are 1/10/2/9 and 3/8/4/7. Next, oligo 3/8/4/7 is ligated to oligo 5/6. The resulting oligo 3/8/4/7/5/6 is then ligated to

oligo 1/10/2/9 resulting in a full length variable region gene. Alternatively, when 12 oligos are used, the order of addition is  $1+12=1/12$ ,  $2+11=2/11$ ,  $3+10=3/10$ ,  $4+9=4/9$ ,  $5+8=5/8$ ,  $6+7=6/7$ ,  $1/12+2/11=1/12/2/11$ ,  $3/10+4/9=3/10/4/9$ ,  $5/8+6/7=5/8/6/7$ ,  $1/12/2/11+3/10/4/9=1/12/2/11/3/10/4/9$ ,

- 5  $1/12/2/11/3/10/4/9+5/8/6/7=1/12/2/11/3/10/4/9/5/8/6/7$ , which is the full length modified variable region gene. The names of oligonucleotides used for construction are listed in Table 7 and Figures 9, , 11, 12C, or 13C.

- Using this method, variable region sequences in which an alanine has been substituted for a cysteine that forms an intrachain disulfide bond can be constructed using  
10 oligonucleotides introducing this change. For example, in constructing the antibody contains the SP-10 portion, oligos SP 3a and SP 4a could be used instead of oligo SP3 or SP4.

- The modified variable region DNA fragment is then cloned into a shuttle vector (e.g. pUC19, *infra*) for sequence analysis and upon sequence confirmation, cloned  
15 into an expression vector. After running the DNA for two hours at 110 volts in a 1% low melting agarose gel, DNA fragments are visualized by ethidium bromide staining and gel slices are cut out and placed in a sterile microfuge tube. Gel purification removes excess free oligomers that may interfere with future ligations. The DNA is eluted from the agarose by addition with f3-Agrase I at 40°C for three hours. DNA is precipitated using 0.3 M  
20 sodium acetate and isopropanol at -20°C for one hour, followed by centrifugation at high speed in a microcentrifuge for ten minutes. Isopropanol is aspirated and the pellet is washed once with 70% ethanol, the sample is spun again and the ethanol is aspirated and the pellet air dried. The DNA pellet is quantitated by running a small fraction of the resuspended pellet (i.e. 1/10th) on a gel and visually comparing to known DNA standards,  
25 or measuring the absorbance of UV light at 260 nM. If the quantity of DNA is to limiting for cloning at this point, it can be amplified by PCR techniques well known to those skilled in the art.

## 7.2 LIGATION OF THE MODIFIED CDR INTO PUC19

- 30 Purified DNA corresponding to the engineered variable region gene is subsequently inserted into the pUC19 vector by ligation. The pUC19 vector is a 2686 base

Table 7

	Oligo 1	Oligo 2	Oligo 3	Oligo 4	Oligo 5	Oligo 6	Oligo 7	Oligo 8	Oligo 9	Oligo 10	Oligo 11	Oligo 12
MSA 1	LDR	DSABL-1	MSAL- CDR1-1	HMV13	HMV14	HMV15	HMV16	HMV17	HMV18	MSAL- CDR1-1c	DSABL-1c	ANTIL DR
MSA1VA C	LDR	DSABL-1	MSALVA C-CDR1- 1	HMV13	HMV14	HMV15	HMV16	HMV17	HMV18	MSALVAC -CDR1-1	DSABL-1c	ANTIL DR
ConVH1	BKHC1	BKHC2	BKHC3	BKHC4	BKHC5	BKHC6	BKHC7	BKHC8	BKHC9	BKHC10		

pair, high copy number *E. coli* plasmid containing a 54 base pair polylinker cloning site in the middle of the lacZ gene. The pUC19 vector also contains an ampicillin resistance marker for selection of bacteria containing the plasmid. The pUC19 is digested with the restriction enzyme *Hinc II* (10 µg plasmid in 50 units enzyme). The resulting blunt ends are  
 5 dephosphorylated with calf intestinal phosphatase (CIP, 2 units in alkaline buffer, 30 minutes at 37°C), to prevent recircularization during the ligation step. The phosphatase is removed by extraction with phenol and chloroform, followed by precipitation with sodium acetate and ethanol on ice for 1 hour. The precipitated DNA is pelleted by high speed centrifugation and the ethanol is removed by aspiration, followed by a washing step with  
 10 70% ethanol to remove excess salts. The DNA pellet is air dried to completely remove any ethanol. The digested, phosphatased vector is then resuspended in TE buffer to 0.5 µg/µl. Approximately 0.1-0.5 µg of vector is incubated with a ten fold molar excess of the constructed variable region containing the sperm cell epitope in the CDR (modified variable region) with T<sub>4</sub> ligase (1000 units) in appropriate buffer and incubated at 16°C for 12 hours.

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### 7.3 BACTERIAL TRANSFORMATION

The ligation mixture containing the engineered variable region gene cloned into pUC19, is transformed into competent bacterial cells. Specifically, 50 µl of freshly prepared competent DH5-α cells are mixed with the ligation mixture of pUC19 and  
 20 modified variable region DNA and transferred to an electroporation cuvette (0.2 cm gap; Bio-Rad). Each cuvette is pulsed at 2.5 kV/200 ohm/25 µF in an electroporator (Bio-Rad Gene Pulser). Immediately thereafter, 1 ml of SOC media is added to each cuvette and cells are allowed to recover for 1 hour at 37°C in centrifuge tubes. An aliquot of cells from each transformation is removed, diluted 1:100, then 100 µl is plated onto LB plates with  
 25 ampicillin (Amp 40 µg/ml). The plates are then incubated at 37°C overnight and only cells containing a plasmid grow.

The plasmid DNA is analyzed after isolation from single colonies picked by sterile toothpick and grown up overnight in 3 ml LB/Amp in a sterile glass test tube, with constant shaking at 37°C. The plasmid DNA is isolated using Easy Prep columns  
 30 (Pharmacia Biotech) and suspended in 100 µl of TE buffer. To confirm the presence of insert, isolated plasmid DNA is digested with *Hinc II* and the digestion product is analyzed by 1.2% agarose gel electrophoresis in Tris-Acetate EDTA buffer (TAE). DNA is stained in the gel with ethidium bromide and visualized under UV light. The colonies that correspond to plasmids with insert are selected for further analysis.

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#### 7.4 DNA SEQUENCING

DNA sequencing is performed to verify the accuracy of the sequence in the cloned fragment. Sequencing across the pUC19 polylinker is done using the M13/pUC universal forward and universal reverse primers using the Sanger dideoxy chain termination  
 5 procedure. The M13/pUC universal primers are readily found in biotechnology supply catalogues. Sequencing is performed on the ABI377 DNA sequencer, and sequence comparison is performed using standard computer alignment programs or visual inspection.

#### 7.5 CLONING INTO THE V<sub>H</sub> AND V<sub>L</sub> CHAIN CONSTRUCTS

10 Once the sequence of the modified CDR has been confirmed, it is cut out of the pUC19 plasmid and ligated into either the heavy or light chain antibody expression vectors pMRRO10.1 or pGAMMA1, respectively (See Figures 6A and B). Alternatively, both the heavy and light chain genes are expressed on the same plasmid, and the modified CDR is ligated into either the heavy or light chain variable region as appropriate.

15 A complete antibody light chain has both a variable region and a constant region. A complete antibody heavy chain contains a variable region, a constant region, and a hinge region. The synthetic variable region genes of the invention are inserted into vectors containing appropriate constant regions. Engineered variable region genes with the sperm antigen epitope sequences are cloned into the pMRRO10.1 vector. The pMRRO10.1  
 20 vector contains a human kappa light chain constant region. Insertion of the engineered light chain variable region into this vector gives a complete light chain sequence. Alternatively, the engineered variable region gene with the sperm antigen sequence, of the heavy chain is inserted into the pGAMMA1 vector. The pGAMMA1 vector contains human and IgG1 constant region and hinge region sequences. Insertion of the engineered heavy chain  
 25 variable region gene into this vector gave a complete heavy chain sequence.

In order to engineer a mammalian vector comprising both heavy chain and light chain genes, the complete light chain sequence and heavy chain sequence were inserted into a mammalian expression vector pNEPuDGV (Figure 6C; Bebbington, C., 1991, In METHODS: A Companion to Methods in Enzymology, 2:136-145). The  
 30 resulting vector encodes both light chain and the heavy chain of the antibody.

#### 7.6 TRANSFECTION OF EUKARYOTIC CELLS

The antibody expression plasmid, pNEPuDGV, is then transfected into a suitable host cell for expression of the antibody of interest. COS-7 (an African green  
 35 monkey kidney cell line, CV-1, transformed with an origin defective SV40 virus), 293, or CHO cells are capable of being transfected and support expression of foreign proteins.



The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the  
5 scope of the appended claims.

Various references are cited herein, the disclosures of which are incorporated by reference in their entireties.

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8. The vaccine composition according to claim 1, wherein said variable region is a heavy chain variable region and said amino acid residue that does not have a sulfhydryl group is at a position corresponding to position 22 or 92 in said heavy chain variable region of said second immunoglobulin molecule.

5

9. The vaccine composition according to claim 1, 7 or 8, wherein said amino acid residue is alanine.

10. The vaccine composition according to claim 1, in which said first immunoglobulin molecule is of a type selected from the group consisting of IgG, IgE, IgM, IgD and IgA.

11. A vaccine composition comprising an amount of a fragment of a first immunoglobulin molecule sufficient to induce an anti-idiotypic response, said first immunoglobulin molecule comprising a variable region and being identical, except for one or more amino acid substitutions in said variable region, to a second immunoglobulin molecule, said second immunoglobulin molecule having at least one complementarity determining region (CDR) that has a portion of an antigen of a cell or protein involved in reproductive function, said one or more amino acid substitutions being the substitution of one or more amino acid residues that do not have a sulfhydryl group at one or more positions corresponding to one or more cysteine residues that form a disulfide bond in said second immunoglobulin molecule; and a pharmaceutically acceptable carrier.

12. The vaccine composition according to claim 11, wherein said antigen is a sperm antigen.

13. The vaccine composition according to claim 12, wherein said sperm antigen is SP-10, MSA-63 or LDH-C4.

14. The vaccine composition according to claim 11, wherein said antigen is selected from the group consisting of gonadotropin-releasing hormone, a gonadotropin, prostaglandin F2 alpha, oxytocin, gonadotropin receptors, SP-17, PH-20, FA-1, FA-2, PH-30, RSA, HAS-63, ZP1, ZP2, and ZP3.

15. The vaccine composition according to claim 11, wherein a first CDR contains a portion of an antigen of a cell or protein associated with reproductive function

and a second CDR contains a portion of an antigen of a cell or protein associated with reproductive function.

16. The vaccine composition according to claim 15, wherein said first CDR  
5 contains a portion of SP-10 antigen, and said second CDR contains a portion of LDH-C4.

17. The vaccine composition according to claim 11, wherein said variable region  
is a light chain variable region and said amino acid residue that does not have a sulfhydryl  
group is at a position corresponding to position 23 or 88 in said light chain variable region of  
10 said second immunoglobulin molecule.

18. The vaccine composition according to claim 11, wherein said variable region  
is a heavy chain variable region and said amino acid residue that does not have a sulfhydryl  
group is at a position corresponding to position 22 or 92 in said heavy chain variable region  
15 of said second immunoglobulin molecule.

19. The vaccine composition according to claim 11, 17 or 18, wherein said  
amino acid residue is alanine.

20. The vaccine composition according to claim 11, in which said first  
20 immunoglobulin molecule is of a type selected from the group consisting of IgG, IgE, IgM,  
IgD and IgA.

21. A method of contraception in a subject comprising administering to said  
25 subject an amount of a first immunoglobulin molecule sufficient to induce an anti-idiotypic  
response, said first immunoglobulin molecule comprising a variable region and being  
identical, except for one or more amino acid substitutions in said variable region, to a  
second immunoglobulin molecule, said second immunoglobulin molecule having at least  
one complementarity determining region (CDR) that has a portion of an antigen of a cell or  
30 protein involved in reproductive function, said one or more amino acid substitutions being  
the substitution of one or more amino acid residues that do not have a sulfhydryl group at  
one or more positions corresponding to one or more cysteine residues that form a disulfide  
bond in said second immunoglobulin molecule.

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22. The method according to claim 21 which further comprises isolating an antibody from said subject, said antibody recognizing the idiotype of said second immunoglobulin molecule and administering said antibody to a second subject.
- 5 23. The method according to claim 21, wherein said antigen is a sperm antigen.
24. The method according to claim 23, wherein said sperm antigen is SP-10, MSA-63 or LDH-C4.
- 10 25. The method according to claim 21, wherein said antigen is selected from the group consisting of gonadotropin-releasing hormone, a gonadotropin, prostaglandin F2 alpha, oxytocin, gonadotropin receptors, SP-17, PH-20, FA-1, FA-2, PH-30, RSA, HAS-63, ZP1, ZP2, and ZP3.
- 15 26. The method according to claim 21, wherein a first CDR contains a portion of an antigen of a cell or protein associated with reproductive function and a second CDR contains a portion of an antigen of a cell or protein associated with reproductive function.
27. The method according to claim 26, wherein said first CDR contains a portion  
20 of SP-10 antigen, and said second CDR contains a portion of LDH-C4.
28. The method according to claim 21, wherein said variable region is a light chain variable region and said amino acid residue that does not have a sulfhydryl group is at a position corresponding to position 23 or 88 in said light chain variable region of said second  
25 immunoglobulin molecule.
29. The method according to claim 21, wherein said variable region is a heavy chain variable region and said amino acid residue that does not have a sulfhydryl group is at a position corresponding to position 22 or 92 in said heavy chain variable region of said  
30 second immunoglobulin molecule.
30. The method according to claim 21, 28 or 29, wherein said amino acid residue is alanine.
- 35 31. The method according to claim 21, in which said first immunoglobulin molecule is of a type selected from the group consisting of IgG, IgE, IgM, IgD and IgA.

**ABSTRACT**

The invention provides an antibody contraceptive vaccine comprising an antibody that has at least one CDR containing a portion of an antigen of a cell or protein associated with reproductive function and which antibody has an enhanced ability to elicit an anti-idiotypic response, for example, by substituting one or more variable region cysteine residues that form intrachain disulfide bonds with an amino acid residue that does not have a sulfhydryl group, such that the intrachain disulfide bond does not form. The invention further provides methods contraception using the antibody contraceptive vaccines of the invention

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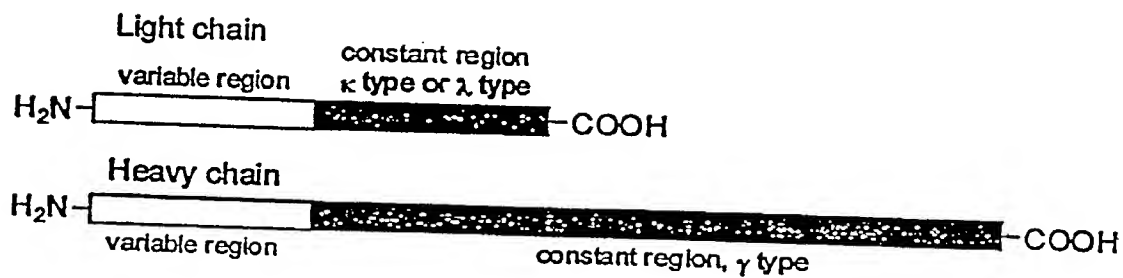


FIG. 1

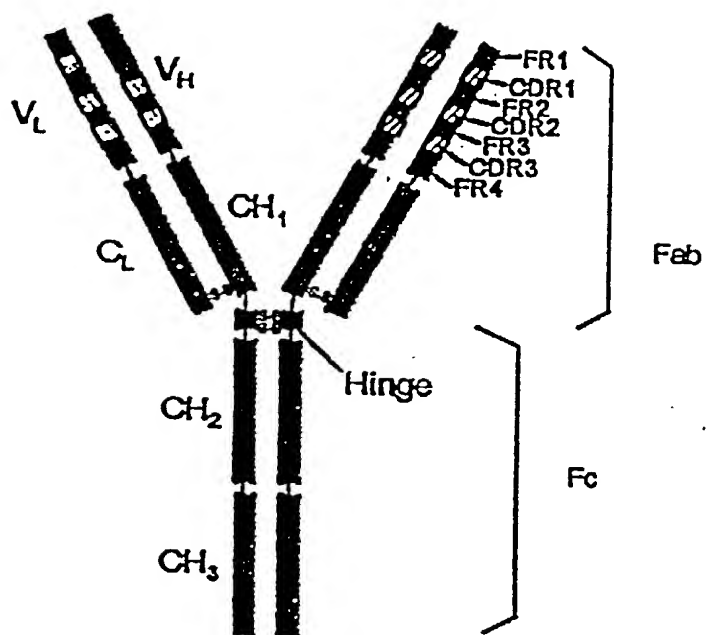


FIG. 2

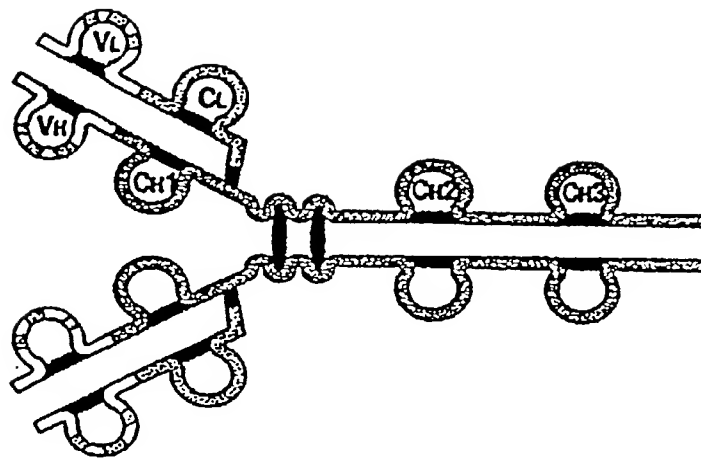
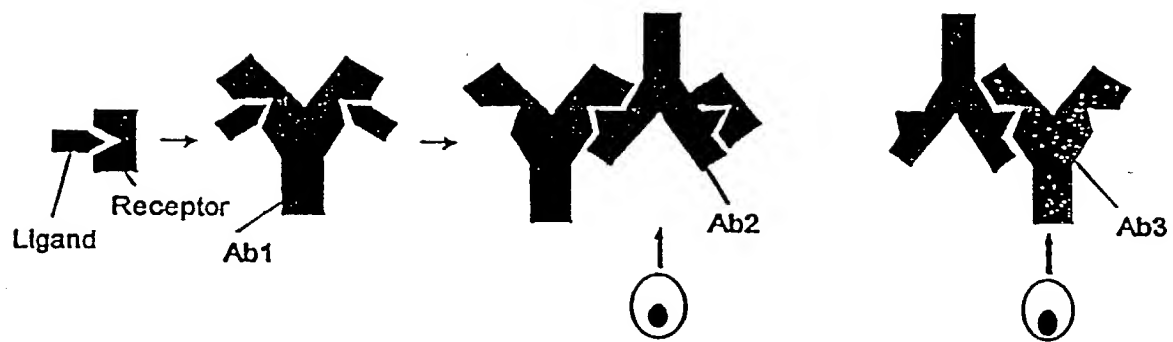


FIG. 3

**FIG. 4**

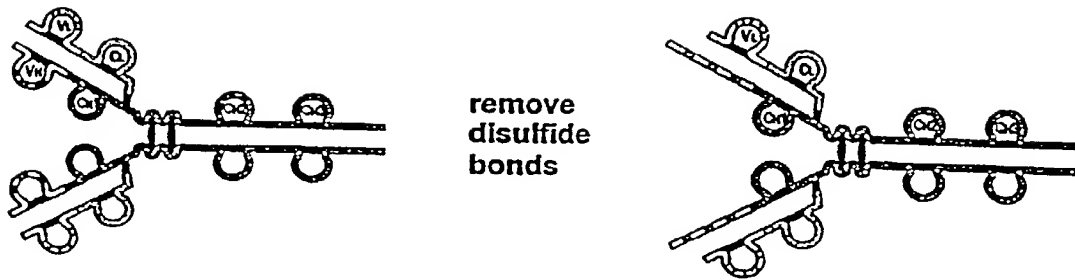


FIG. 5

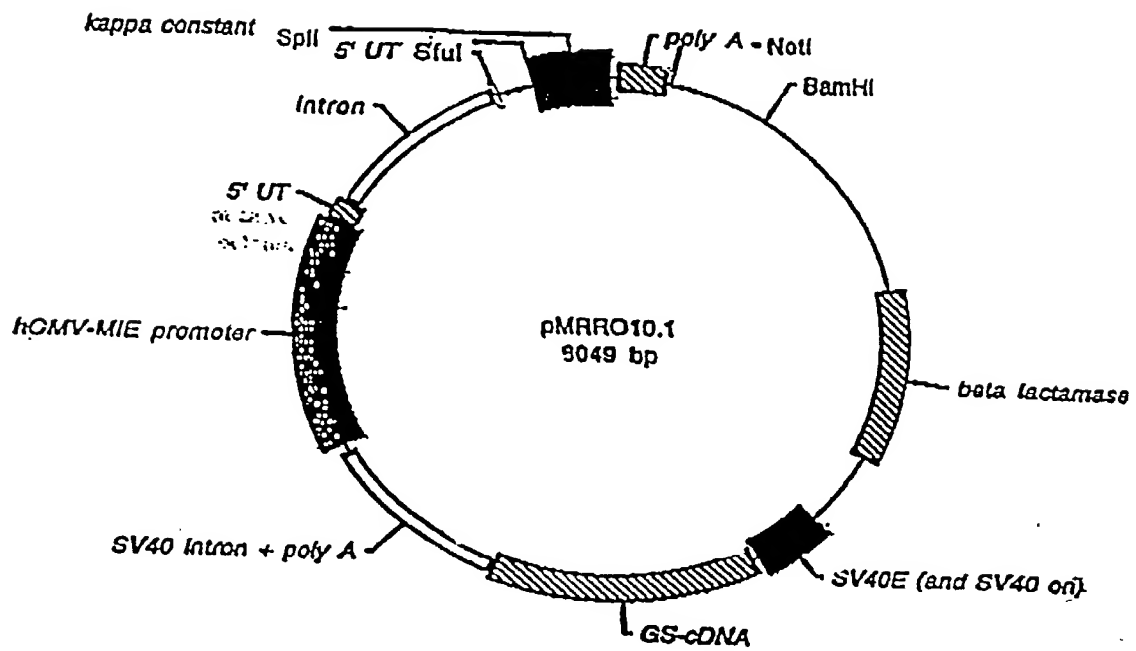


FIG. 6A

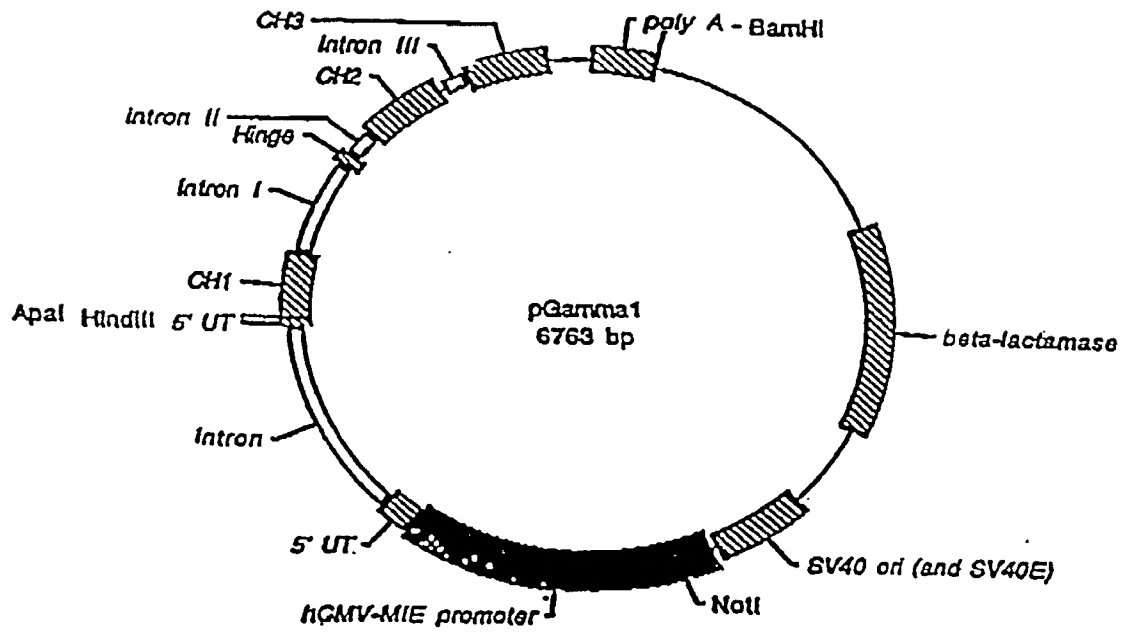


FIG. 6B

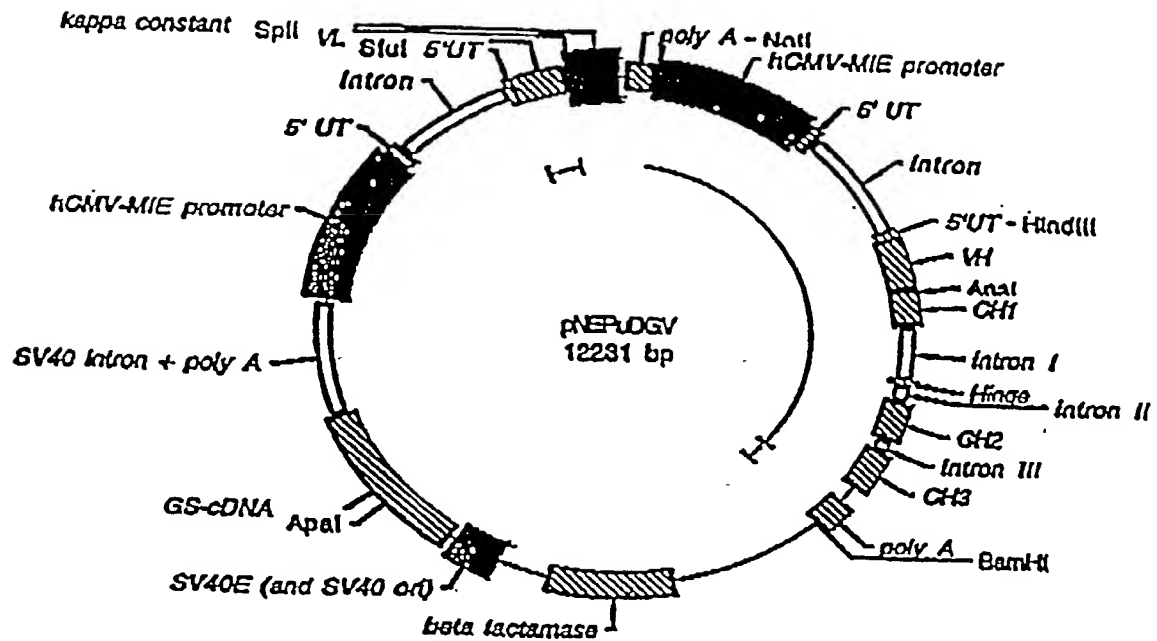


FIG. 6C

WO 00/29443

PCT/US99/26671

9/20

ConvL1

EcoRI  
GAA TTC

6

-19 (Leader)

Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser Ala Gln Ala  
 ATG GCT TGG GTG TGG ACC TTG CTA TTC CTG ATG GCA GCT GCC CAA AGT GCC CAA GCA  
 63

VL:

1 10 20  
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val  
 Thr  
 GAT ATC CAA ATG ACA CAA AGT CCT AGT AGT TTG AGT GCT AGT GTG GGA GAT CGG GTG  
 ACA 123

21 30 40  
 Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys  
 Pro  
 ATC ACA TGT CGG GCT AGT CAA AGT ATC AGT AAC TGT TTG GCT TGG TAT CAA CAA AAG  
 CCT 183

41 50 60  
 Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro  
 Ser  
 GGA AAG GCT CCT AAG TTG TTG ATC TAT GCT GCT AGT AGT TTG GAG AGT GGA GTG CCT  
 AGT 243

61 70 80  
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Arg Phe Thr Leu Thr Ile Ser Ser Leu Gln  
 Pro  
 OGG TTC AGT GGA AGT GGA AGT GGA ACA OGG TTC ACC TTG ACC ATC AGT AGT TTG CAA  
 CCT 303

81 90 100  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Leu Pro Trp Thr Phe Gly  
 Gln  
 GAG CAT TTC GCT ACC TAT TAT TGT CAA CAA TAT AAC AGT TTG CCT TGG ACC TTC GGA  
 CAA 363

101  
 Gly Thr Lys Val Glu Ile Lys  
 GGA ACC AAG GTG GAG ATC AAG GAA TTC  
 Eco RI

390

FIG. 7A

WO 00/29443

PCT/US99/26671

10/20

ConVH1

EcoRI  
GAA TTC

6

-19 (Leader)

-1

Met Ala trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala  
 Gln Ser Ala Gln Ala  
 ATG GCT TGG GTG TGG ACC TTG CTA TTC CTG ATG GCA GOT GCC  
 CAA AGT GCC CAA GCA 63

VL:

1 10 20  
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro  
 Gly Ala Ser Val Lys Val  
 CAG GTT CAG CTG GTG CAG TCT GGC GCT GAG GTG AAG AAG CCT  
 GGC GCT TCT GTG AAG GTG 123

21:

30

35A 35B

40  
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Ala Ile  
 Ser Trp Asn Trp Val Arg Gln Ala  
 TCT TGC AAG GCT TCT GGC TAC ACA TTC ACA TCT TAC GCT ATA  
 TCT TGG AAT TGG GTG AGG CAG GCT 189

41

50

60

Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Gly Asn  
 Gly Asp Thr Asn Tyr Ala  
 CCT GGC CAG GGC CTG CAG TGG ATG GGC TGG ATA AAT GGA AAT  
 GGA GAT ACA AAT TAC GCC 249

61

70

80

Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser  
 Thr Ser Thr Ala Tyr Met  
 CAG AAG TTC CAG GGA AGG GTG ACT ATA ACT GCT GAT ACT TCT  
 ACT TCT ACT GCT TAC ATG 309

81

82A 82B 82C

90

100  
 Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr  
 Cys Ala Arg Ala Pro Gly Tyr Gly Ser  
 GAG CTG TCT TCT CTG AGG TCT CAG GAT ACT GCT GTT TAC TAC  
 TGC GCT AGG GCT CCT GGC TAC GGC TCT 378

101

110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 CAT TAT TGG GGA CAG GGA ACA CTG GTT ACA GTT TCT TCT GAA TTC  
 423

FIG. 7B

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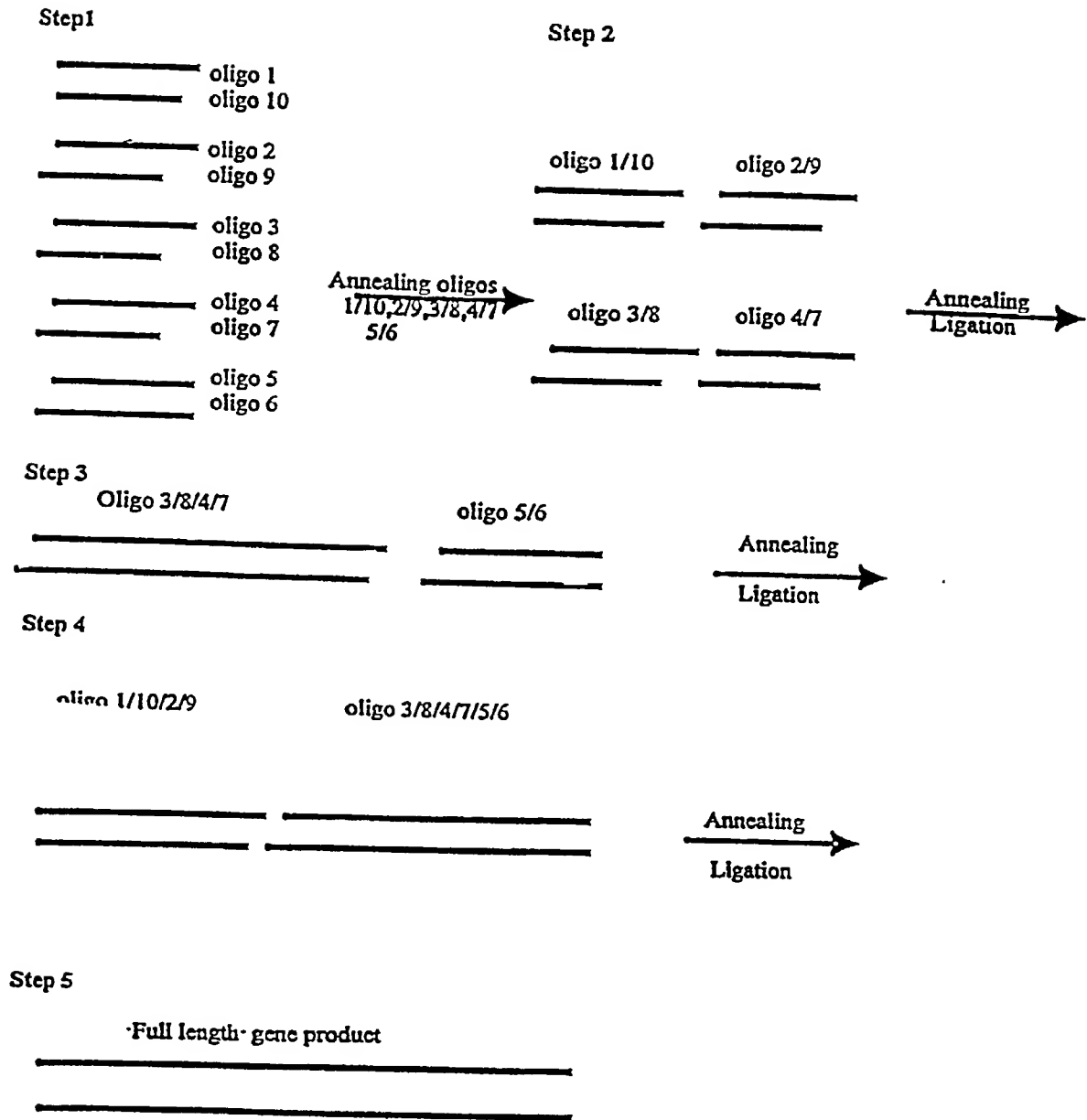


FIG. 8

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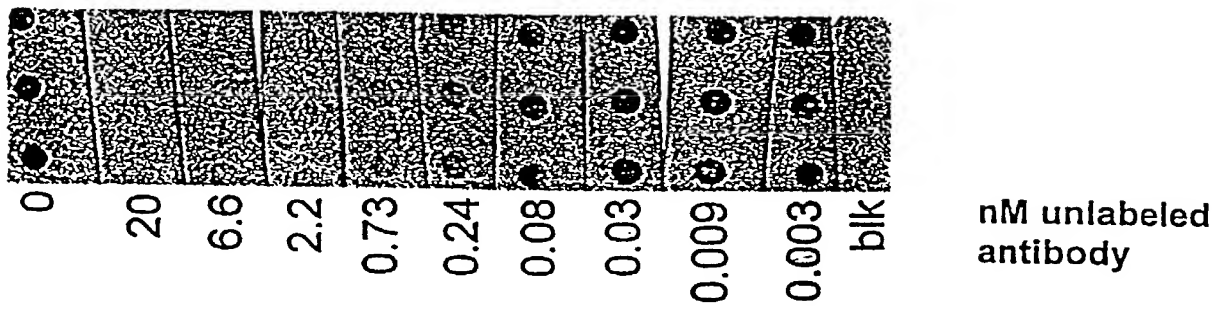
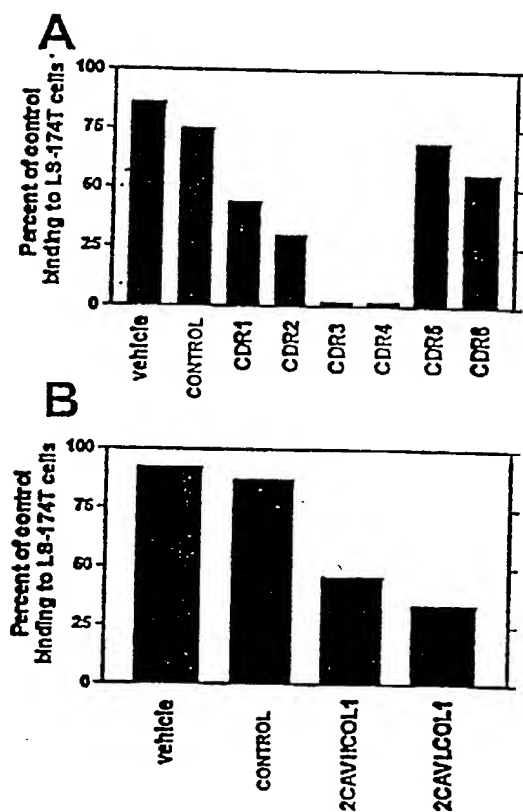


FIG. 9

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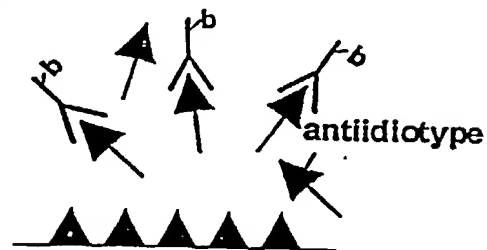
13/20



**C**



**D**



FIGS. 10A-D

cstrcy  
 DSABL-1 GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTGTCAGTTGGAGAGAAGGTTACTATG 0.05  
 PAGE 83  
 DSABL-1c  
 GCAGCTCATAGTAACCTTCTCTCCAACCTGACACAGCTAGGGAGGATGGAGACTGTGACATCACAATGTCTGC  
 TTGGGC 0.05 PAGE 78  
 MSAL-CDR1-1 *ECT in MSAL VAC-CDR1-1*  
 AGCTGGCTCGGCAGCCTCCGAAGCAGCCCCGCTCCAGAGCCCCGCTGCTCCGATGGTACCAGCAGAAACCAG  
 GGCAGTCTCCTAAA 0.05 PAGE 84  
 MSAL-CDR1-1c  
 CTGCCCTGGTTTCTGCTGGTACCATCGGAGCAGCGGGCTCTGGAGCGGGGCTGCTTCCGGAGGCTGCCGAC  
 0.05 PAGE 89

HMV1 GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTGTCAGTTGGAGAGAAGGTTACTATGAGCCCTAAGTCCAGT  
 HMV2 CAGAGCCCTTTTATATAGTACCAATCAAAAGATCTACTTGGCCTGGTACCAGCAGAACCAAGCCAGTCTCCTAAA  
 HMV3 CTGCTGATTTACTGGCATCCACTAGGGAATCTGGGCTCCTGATCGCTTCAGAGGCGGTGATCTGGG  
 HMV4 GCACAGCATAATATAGATATCCTCCGAGCTTCCTGGAGGACCAAGCTGGAAATCAAGCGGATTC  
 HMV5 ACCGCTCTGAGCGATCAGGGAAGCCAGATTCCTAGTGGATGCCAGTAAATCAGGATTTAGGAGA  
 HMV6 CTGCCCTGGTTCTCTGCTACAGGCCAAGTACATCTTTGATTCCTACTATATAAAGCCTCTGACTGGCTT  
 HMV10 AGCCCTCATATAGCTTCTCTCCAGTACAGCTAGGAGGATGAGAGCTGTGACATCACAATGTCTCCTTGGGC  
 HMV16 CAATTCGCTTTCATTCAGCTTGGTCCCTCCAGCAAGCTCCGAGGATATCTATAATATGCTGTGGTAAATAC

HMVL4

AGG AGA TTT CAG TCT CAG CAT CAG CAG TGT GAA GGG TGA AGA COT GGG  
 AGT TTA TTA C

HMVL7

TG CCA GGT CTT CAG COT TCA CAG TGO TGA TGG TGA GAG TGA AAT CTG  
 TCC CAG ATC C

FIG. 11

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- A** MSA-63 epitope DNA  
 GTC GGC AGC CTC CGA AGC AGC CCG CTC CAG AGC CCG CTG CTC CGA CCG CTC GTC  
 CAG AGC AGC CTC TGC TTG CTG TTC CTC TTG CTG CGA TAC AGC TGC GGC GAC GGC AGC  
 TGC AGC CGA CGA TAC TGC GAC TTG ACG GTG TGC ACG CGA ATG TAC TTG CTG CTG  
 CGA TTC ACG GAC GCG CCG CTC CCG CAG ACG TGC TGC GTC TTG AGC
- B** MSA-63 protein sequence (Start residue 143 end residue 233)  
 Gln Pro Ser Glu Ala Ser Ser Gly Glu Val Ser Gly Asp Glu Ala Gly Glu Gln Val Ser Ser Glu Thr Asn Asp  
 Lys Glu Asn Asp Ala Met Ser Thr Pro Leu Pro Ser Thr Ser Ala Ala Ile Thr Leu Asn Cys His Thr Cys Ala  
 Tyr Met Asn Asp Asp Ala Lys Cys Leu Arg Gly Glu Gly Val Cys Thr Thr Gln Asn Ser
- C** MSA-63 oligo
- MSA1  
 GTC GGC AGC CTC CGA AGC AGC CCG CTC CAG AGC CCG CTG CTC CGA
- MSA2  
 AGC CCG CTG CTC CGA CCG CTC GTC CAG AGC AGC CTC TGC TTG CTG
- MSA3  
 AGC CTC TGC TTG CTG TTC CTC TTG CTG CGA TAC AGC TGC GGC GAC
- MSA4  
 TAC AGC TGC GGC GAC GGC AGC TGC AGC CGA CGA TAC TGC GAC TTG
- MSA5  
 CGA TAC TGC GAC TTG ACG GTG TGC ACG CGA ATG TAC TTG CTG CTG
- MSA6  
 ATG TAC TTG CTG CTG CGA TTC ACG GAC GCG CCG CTC CCG CAG ACG
- MSA7  
 CGA TTC ACG GAC GCG CCG CTC CCG CAG ACG TGC TGC GTC TTG AGC

FIGS. 12A-C

- A** SP-10 Epitope  
 GAA TTC CAG CCT TCA GGT GAA CAT GGC TCC GGT GAA CAG CCT TCT GGT GAG CAG  
 GCC TCG GGT GAA CAG CCT TCA GGT GAG CAC GCT TCA GGG GAA CAG GCT TCA GGT  
 3CA CCA ATT TCA AGC ACA TCT ACA GGC ACA ATA TTA AAT TGC TAC ACA TGT GCT TAT  
 ATG AAT GAT CAA GGA AAA TGT CTT CGT GGA GAG GGA ACC TGC ATC ACT CAG AAT TC
- B** SP-10 protein sequence  
 Gln Pro Ser Gly Glu His Gly Glu Gln Pro Ser Gly Glu Gln Ala Ser Gly Glu Gln Pro Ser gly Glu His Ala  
 Ser Gly Glu Gln Ala Ser Gly Ala Gln Ile Ser Ser Thr Ser Thr Gly Thr Ile Leu Asn Cys Tyr Thr Cys Ala  
 Tyr Met Asn Asp Gln Gly Lys Cys Leu Arg Gly Glu Gly Thr Cys Ile Thr Gln Asn
- C** Oligo SP1:  
 GAA TTC CAG CCT TCA GGT GAA CAT GGC TCC GGT GAA CAG CCT TCT GGT GAG CAG  
 GCC TCG GGT GAA CAG CCT TAG
- Oligo SP2:  
 GTG AGC ACG CTT CAG GGG AAC AGG CTT CAG GTG CAC CAA TTT CAA GCA CAT CTA  
 CAG GCA CAA TAT TAA ATT GCT
- Oligo SP3:  
 ACA CAT GTG CTT ATA TGA ATG ATC AAG GAA AAT GTC TTC GTG GAG AGG GAA CCT  
 GCA TCA CTC AGA ATT C
- Oligo SP3a(3Cys->Ala):  
 ACA CAG CAG CTT ATA TGA ATG ATC AAG GAA AAG CAC TTC GTG GAG AGG GAA  
 CCG CAA TCA CTC AGA ATT C
- Oligo SP4:  
 GAA TTC TGA GTG ATG CAG GTT CCC TCT CCA CGA AGA CAT TTT CCT TGA TCA TTC ATA  
 TAA GCA CAT GTG TAG CAA TTT A
- Oligo SP4a (3Cys->Ala):  
 GAA TTC TGA GTG ATT GCG GTT CCC TCT CCA CGA AGT GCT TTT CCT TGA TCA TTC ATA  
 TAA GCT GCT GTG TAG CAA TTT A
- Oligo SP5:  
 ATA TTG TGC CTG TAG ATG TGC TTG AAA TTG GTG CAC CTG AAG CCT GTT CCC CTG AAG  
 CGT GCT CAC CTG AAG GCT
- Oligo SP6:  
 GTT CTC CCG AGG CCT GCT CAC CAG AAG GCT GTT CAC CGG AGC CAT GTT CAC CTG  
 AAG GCT GGA ATT C

FIGS. 13A-C

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**LDH-C<sub>4</sub> Epitope:****Oligo LDH1:**

TCG TGC CAG TTC CTC GTC GAC TAG CTC TTC GAC TAG CTC CTG CTG CTC TTG TCG GTC  
ACG GAA TTC

**Oligo LDH2:**

GAA TTC CGT GAC CGA CAA GAG CAG CAG GAG CTA GTC GAA GAG CTA GTC GAC GAG  
GAA CTG GCA CGA CGG GTT CGT

**FIG. 14**

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Leader:

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Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Gln Ser Ala Gln Ala  
ATG GCT TGG GTG TGG ACC TTG CTA TTC CTG ATG GCA GCT GCC CAA AGT GCC CAA GCA

Plac  
V<sub>1</sub>  
GCT in vaccine

Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly Gln Lys Val Thr  
GAC ATT GTG ATG TCA CAG TCT CCA TCC TCC CTA GCT GTC TCA GTT GGA CAG AAG GTT ACT

Met Ser Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Ser Asn Gln Lys Ile Tyr Leu Ala  
ATG AGC ATC AAG TCC AGT CAG AGC CTT TTA TAT AGT AGC AAT CAA AAG ATC TAC TTG GCC

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Gln Ser Gly Val Pro Asp  
GGG CAG TCT CCT CCA CAG CTG CTG ATT TAC TGG GCA TCC ACT AGG GAA TCT GGG GTC CCT GAT

Arg Phe Thr Gly Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Lys Ala  
CGC TTC ACA GGC GGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT GTG AAG GCT

Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Arg Tyr Pro Arg Thr Phe Gly Gly  
GAA GAC CTG GCA GTT TAT TAC TGT CAG CAA TAT TAT AGA TAT CCT CGG ACG TTC GGT GGA

Gly Thr Lys Leu Gln Ile Lys Arg  
GGC ACC AAG CTG GAA ATC AAA CGG

CDR 1  
CDR 2  
CDR 3

FIG. 15

**2CAVHCOL1**

VHC1 5'GAATTCATGGCTTGGGTGTGGACCTTGCTATTCCTGATGGCAGCTGOCCAAAGTGCC  
AAGCACAGATOCAGTTGGTGCA 3'

VHC2 5'GTCTGGAOCTGAGCTGAAGAAGCCTGGAGAGACAGTCAAGATCTCOGCTAAGGCTTC  
TGGGTATACCTTCACAACTAG 3'

VHC3 5'GAATGAACTGGGTGAAGCAGGCTOCAGGAAAGGGTTTAAAGTGGATGGGCTGGAT  
AAACACCTACACTGGAGAGOCAACA 3'

VHC4 5'TATGCTGATGACTTCAAGGGACGGTTTGCTTCTCTTTGGAAAOCTCTGOCAGCACT  
GOCTATTGTCAGATCAACAOC 3'

VHC5 5'CAAAAATGAGGACAOGGCTACATATTTGCTGCAAGAGOCCTACTATGGTAAATAC  
TTTGACTACGAATTC 3'

VHC6 5'GAATTGCTAGTCAAAGTATTTAOCATAGTAGGCTCTTGCAGCAAATATG 3'

VHC7 5'TAGCOGTGTCTCATTCTTTGAGGTTGTTGATCTGCAAATAGGCAGTGCTGGCAGA  
GGTTTCCAAAGAGAAGGCAAACCGT 3'

VHC8 5'CCCTTGAAGTCATCAGCATATGTTGGCTCTOCAGTGTAGGTGTTTATCCAGCCAT  
CCACTTTAAACCCCTTCTCTGGAGC 3,

VHC9 5'CTGCTTCAOCCAGTTCAATOCATAGTTTGTGAAGGTATACCCAGAAGCCTTAGCGG  
AGATCTTGACTGTCTCTOCAGGCT 3'

VHC10 5'TCTTCAGCTCAGGTCCAGACTGCCAACCTGGATCTGTGCTTGGGCACTTTG GGC  
AGCTGOCATCAGGAATAGCAAGGTCCACACCCAAGCCATGAATTC 3'

**FIG. 16A**

**2CAVLCOL1**

VLC1 5'AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTT  
ACCATA 3'

VLC2 5'ACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAAACC  
AGGGCAG 3'

VLC3 5'TCTCCTAAACTGCTGATATACTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCT  
TCACTGGCAGT 3'

VLC4 5'GGATATGGGACGGATTTCACCTTTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCA  
GTTTAT 3'

VLC5 5'TTCTGYCAGCAGGATTATAGCTCTCCGCTCACGTTCCGGTGCTGGGAACCAAGCTGGAG  
CTGAAAGAATTC 3'

VLC6 5'GAATTCTTTCAGCTCCAGCTTGGTCCCAGCAACCGAACGTGAGCGGAGAGCTATAATC  
CTGCTGACAGAAATAAACTGC 3'

VLC7 5'CAGGTCTTCAGCCTGCACAGTGCTGATGGTGAAAGTGAAATCCGTCCCATATCCA  
CTGCCAGT 3'

VLC8 5'GAAGCGATCAGGGACTCCAGTGTAGCGATTGGATGCATAGTATATCAGCAGTTAG  
GAGACTGCCCTGG 3'

VLC9 5'TTCTGTGGTACCAAGCTACATCATTACTCACACTCTGACTGGCCTTGCAGGTTA  
TGGTAAC 3'

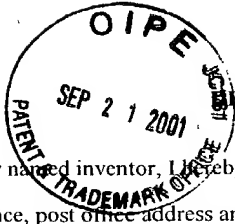
VLC10 5'CCTGTCTCTGCTGATACAAGCAGGAATTTGGGAGTCTGGGTCATCACAATACTT  
GCTTGGGC 3'

VLC11 5'TTCGCTCAGCAGGATTATAGCTCTCCGCTCACGTTCCGGTGCTGGGAACCAAGCTGG  
AGCTGAAAGAATC 3'

VLC12 5'GAATTCTTTCAGCTCCAGCTTGGTCCCAGCAACCGAACGTGAGCGGAGAGCTATAA  
TCCTGCTGAGCGAAATAAACTGC 3'

**FIG. 16 B**

13 SEP 2001 15:33:31



## DECLARATION FOR NON-PROVISIONAL PATENT APPLICATION\*

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below at 201 et seq. beneath my name.

I believe I am the original, first and sole inventor if only one name is listed at 201 below, or an original, first and joint inventor if plural names are listed at 201 et seq. below, of the subject matter which is claimed and for which a patent is sought on the invention entitled

## CONTRACEPTIVE ANTIBODY VACCINES

and for which a patent application:

☐ is attached hereto and includes amendment(s) filed on (if applicable)

☒ was filed in the United States on May 10, 2001 as Application No. 09/831,631 with amendment(s) filed on May 10, 2001.

☒ was filed as PCT international Application No. PCT/US99/26671 on November 12, 1999 and was amended under PCT Article 19 on (if applicable)

I hereby state that I have reviewed and understand the contents of the above identified application, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, §119(a)-(d) of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED PRIOR TO THE FILING DATE OF THE APPLICATION			
APPLICATION NUMBER	COUNTRY	DATE OF FILING (day, month, year)	PRIORITY CLAIMED
			YES <input type="checkbox"/> NO <input type="checkbox"/>
			YES <input type="checkbox"/> NO <input type="checkbox"/>
			YES <input type="checkbox"/> NO <input type="checkbox"/>

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional application(s) listed below.

PROVISIONAL APPLICATION NUMBER	FILING DATE
60/108,325	November 13, 1998

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code §112, I acknowledge the duty to disclose information known to me which is material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application:

NON-PROVISIONAL APPLICATION SERIAL NO.	FILING DATE	STATUS		
		PATENTED	PENDING	ABANDONED

\* for use only when the application is assigned to a company, partnership or other organization.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

201	FULL NAME OF INVENTOR	LAST NAME Burch	FIRST NAME Ronald	MIDDLE NAME Martin
	RESIDENCE & CITIZENSHIP	CITY Wilton	STATE OR FOREIGN COUNTRY Connecticut	COUNTRY OF CITIZENSHIP U.S.A.
	POST OFFICE ADDRESS	STREET 12 Powderhorn	CITY Wilton	STATE OR COUNTRY Connecticut ZIP CODE 06897
		SIGNATURE OF INVENTOR 201 <i>Ronald Martin Burch</i>		DATE 18 August 2001
202	FULL NAME OF INVENTOR	LAST NAME Sackler	FIRST NAME David	MIDDLE NAME Alex
	RESIDENCE & CITIZENSHIP	CITY Greenwich	STATE OR FOREIGN COUNTRY Connecticut	COUNTRY OF CITIZENSHIP U.S.A.
	POST OFFICE ADDRESS	STREET 25 Windrose Way	CITY Greenwich	STATE OR COUNTRY Connecticut ZIP CODE 06830
		SIGNATURE OF INVENTOR 202		DATE
203	FULL NAME OF INVENTOR	LAST NAME	FIRST NAME	MIDDLE NAME
	RESIDENCE & CITIZENSHIP	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF CITIZENSHIP
	POST OFFICE ADDRESS	STREET	CITY	STATE OR COUNTRY ZIP CODE
		SIGNATURE OF INVENTOR 203		DATE
204	FULL NAME OF INVENTOR	LAST NAME	FIRST NAME	MIDDLE NAME
	RESIDENCE & CITIZENSHIP	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF CITIZENSHIP
	POST OFFICE ADDRESS	STREET	CITY	STATE OR COUNTRY ZIP CODE
		SIGNATURE OF INVENTOR 204		DATE
205	FULL NAME OF INVENTOR	LAST NAME	FIRST NAME	MIDDLE NAME
	RESIDENCE & CITIZENSHIP	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF CITIZENSHIP
	POST OFFICE ADDRESS	STREET	CITY	STATE OR COUNTRY ZIP CODE
		SIGNATURE OF INVENTOR 205		DATE

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

2 0 1	FULL NAME OF INVENTOR	LAST NAME Burch	FIRST NAME Ronald	MIDDLE NAME Martin	
	RESIDENCE & CITIZENSHIP	CITY Wilton	STATE OR FOREIGN COUNTRY Connecticut	COUNTRY OF CITIZENSHIP U.S.A.	
	POST OFFICE ADDRESS	STREET 12 Powderhorn	CITY Wilton	STATE OR COUNTRY Connecticut	ZIP CODE 06897
		SIGNATURE OF INVENTOR 201		DATE	
		<i>[Signature]</i>			
2 0 2	FULL NAME OF INVENTOR	LAST NAME Sackler	FIRST NAME David	MIDDLE NAME Alex	
	RESIDENCE & CITIZENSHIP	CITY Greenwich	STATE OR FOREIGN COUNTRY Connecticut	COUNTRY OF CITIZENSHIP U.S.A.	
	POST OFFICE ADDRESS	STREET 25 Windrose Way	CITY Greenwich	STATE OR COUNTRY Connecticut	ZIP CODE 06830
		SIGNATURE OF INVENTOR 202		DATE	
		<i>David Sackler</i>		8/14/01	
2 0 3	FULL NAME OF INVENTOR	LAST NAME	FIRST NAME	MIDDLE NAME	
	RESIDENCE & CITIZENSHIP	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF CITIZENSHIP	
	POST OFFICE ADDRESS	STREET	CITY	STATE OR COUNTRY	ZIP CODE
		SIGNATURE OF INVENTOR 203		DATE	
2 0 4	FULL NAME OF INVENTOR	LAST NAME	FIRST NAME	MIDDLE NAME	
	RESIDENCE & CITIZENSHIP	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF CITIZENSHIP	
	POST OFFICE ADDRESS	STREET	CITY	STATE OR COUNTRY	ZIP CODE
		SIGNATURE OF INVENTOR 204		DATE	
2 0 5	FULL NAME OF INVENTOR	LAST NAME	FIRST NAME	MIDDLE NAME	
	RESIDENCE & CITIZENSHIP	CITY	STATE OR FOREIGN COUNTRY	COUNTRY OF CITIZENSHIP	
	POST OFFICE ADDRESS	STREET	CITY	STATE OR COUNTRY	ZIP CODE
		SIGNATURE OF INVENTOR 205		DATE	

## POWER OF ATTORNEY

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Ronald Martin BURCH and David Alex SACKLER

Application No.: 09/831,631

Group Art Unit: To be assigned,

Filed: May 10, 2001

Examiner: To be assigned.

For: CONTRACEPTIVE ANTIBODY  
VACCINES

Attorney Docket No.: 6750-018

**POWER OF ATTORNEY BY ASSIGNEE  
AND EXCLUSION OF INVENTOR(S) UNDER 37 C.F.R. 3.71**Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

The undersigned assignee of the entire interest in the above-identified subject application hereby appoints: Berj A. Terzian (Reg. No. 20060), David Weild, III (Reg. No. 21094), Jonathan A. Marshall (Reg. No. 24614), Barry D. Rein (Reg. No. 22411), Stanton T. Lawrence, III (Reg. No. 25736), Charles E. McKenney (Reg. No. 22795), Philip T. Shannon (Reg. No. 24278), Francis E. Morris (Reg. No. 24615), Charles E. Miller (Reg. No. 24576), Gidon D. Stern (Reg. No. 27469), John J. Lauter, Jr. (Reg. No. 27814), Brian M. Poissant (Reg. No. 28462), Brian D. Coggio (Reg. No. 27624), Rory J. Radding (Reg. No. 28749), Stephen J. Harbulak (Reg. No. 29166), Donald J. Goodall (Reg. No. 19766), Thomas E. Friebe (Reg. No. 29258), Laura A. Coruzzi (Reg. No. 30742), Jennifer Gordon (Reg. No. 30753), Geraldine F. Baldwin (Reg. No. 31232), Victor N. Balancia (Reg. No. 31231), Samuel B. Abrams (Reg. No. 30605), Steven I. Wallach (Reg. No. 35402), Marcia H. Sundeen (Reg. No. 30893), Paul J. Zegger (Reg. No. 33821), Edmond R. Bannon (Reg. No. 32110), Bruce J. Barker (Reg. No. 33291), Adriane M. Antler (Reg. No. 32605), Thomas G. Rowan (Reg. No. 34419), James G. Markey (Reg. No. 31636), Thomas D. Kohler (Reg. No. 32797), Scott D. Stimpson (Reg. No. 33607), Gary S. Williams (Reg. No. 31066), Ann L. Gisolfi (Reg. No. 31956), Todd A. Wagner (Reg. No. 35399), Scott B. Familant (Reg. No. 35514), Kelly D. Talcott (Reg. No. 39582), Francis D. Cerrito (Reg. No. 38100), Anthony M. Insogna (Reg. No.

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35203), Brian M. Rothery (Reg. No. 35340), Brian D. Siff (Reg. No. 35679), Alan Tenenbaum (Reg. No. 34939), Michael J. Lyons (Reg. No. 37386), Garland T. Stephens (Reg. No. 37242) and William J. Sipio (Reg. No. 34514), all of Pennie & Edmonds LLP, whose addresses are 1155 Avenue of the Americas, New York, New York 10036, 1667 K Street N.W., Washington, DC 20006 and 3300 Hillview Avenue, Palo Alto, CA 94304, all of Pennie & Edmonds LLP (PTO Customer No. 20583), as its attorneys to prosecute this application and to transact all business in the United States Patent and Trademark Office connected therewith, said appointment to be to the exclusion of the inventors and their attorney(s) in accordance with the provisions of 37 C.F.R. 3.71, provided that, if any one of these attorneys ceases being affiliated with the law firm of Pennie & Edmonds LLP as partner, counsel, or employee, then the appointment of that attorney and all powers derived therefrom shall terminate on the date such attorney ceases being so affiliated.

An assignment of the entire interest in the above-identified subject application:

- ☐ was recorded on \_\_\_\_\_ at reel/frame /\_\_\_\_\_.  
☒ was submitted on May 10, 2001 for recording.

Please direct all correspondence for this application to customer no. 20583.

ASSIGNEE:

Euro-Celtique S.A.

Signature:

Douglas Docherty

Typed Name:

DOUGLAS DOCHERTY

Position/Title:

DIRECTOR

Address:

122. bld. De la Petrusse.

Luxembourg

Date:

SEPTEMBER 28, 2001

# SEQUENCE LISTING

<110> Burch, Ronald  
Sackler, David

<120> Contraceptive Antibody Vaccines

<130> 6750-018-999

<140> 09/831,631

<141> 2001-05-10

<160> 70

<170> PatentIn version 3.0

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<211> 16

<212> DNA

<213> Artificial

<220>

<221> misc\_feature

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aacagctatg accatg 16

<210> 2

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<212> DNA

<213> Artificial

<220>

<221> misc\_feature

<223> Description of artificial sequence: Primer for PCR

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gaattcatgg cttgggtgtg 20

<210> 3

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<212> PRT

<213> Artificial

<220>

<221> misc\_feature

<223> Description of artificial sequence: CDR Drived peptide

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<221> SITE

<222> (1)..(1)

<223> Xaa = biotin

<400> 3  
Xaa Thr Ala Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala  
1 5 10

<210> 4



```

<220>
<221> site
<222> (1)..(1)
<223> Xaa = biotin

<400> 7
Xaa Ala Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp
1          5          10          15
Asp Phe Lys Gly
          20

<210> 8
<211> 12
<212> PRT
<213> Artificial

<220>
<221> misc_feature
<223> Description of artificial sequence: CDR Drived peptide

<220>
<221> site
<222> (1)..(1)
<223> Xaa = biotin

<400> 8
Xaa Ala Arg Ala Tyr Tyr Gly Lys Tyr Phe Asp Tyr
1          5          10

<210> 9
<211> 221
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description of Artificial Sequence: Sperm cell specific epitope

<400> 9
gaattccagc cttcaggtga acatggctcc ggtgaacagc cttctggtga gcaggcctcg      60
ggtgaacagc cttcaggtga gcacgcttca ggggaacagg cttcaggtgc accaatttca      120
agcacatcta caggcacaat attaaattgc tacacatgtg cttatatgaa tgatcaagga      180
aatgtcttc gtggagaggg aacctgcac cactcagaatt c                          221

<210> 10
<211> 69
<212> PRT
<213> Artificial

<220>
<221> misc_feature
<223> Description of Artificial Sequence: Sperm cell specific epitope

<400> 10
Gln Pro Ser Gly Glu His Gly Glu Gln Pro Ser Gly Glu Gln Ala Ser
1          5          10          15
Gly Glu Gln Pro Ser Gly Glu His Ala Ser Gly Glu Gln Ala Ser Gly
          20          25          30
Ala Gln Ile Ser Ser Thr Ser Thr Gly Thr Ile Leu Asn Cys Tyr Thr
          35          40          45

```



```

<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description of Artificial Sequence: Cloning primers for SP10

<400> 15
gaattctgag tgatgcaggt tccctctcca cgaagacatt ttccttgatc attcatataa    60
gcacatgtgt agcaattta                                                    79

<210> 16
<211> 79
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description of Artificial Sequence: Cloning primers for SP10

<400> 16
gaattctgag tgattgcggt tccctctcca cgaagtgttt tttgatgatc attcatataa    60
gtgtgtgtgt agcaattta                                                    79

<210> 17
<211> 75
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description of Artificial Sequence: Cloning primers for SP10

<400> 17
atattgtgcc tgtagatgtg cttgaaattg gtgcacctga agcctgttcc cctgaagcgt    60
gtcacctga agcct                                                    75

<210> 18
<211> 67
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description of Artificial Sequence: Cloning primers for SP10

<400> 18
gttctcccga ggctgtgtca ccagaaggct gttcaccgga gccatgttca cctgaaggct    60
ggaattc                                                            67

<210> 19
<211> 210
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description of Artificial Sequence: Sperm cell specific epitope M

```

## SA-6

<400>	19						
gtcggcagcc	tccgaagcag	cccgcctccag	agccccgctgc	tccgaccgct	cgtccagagc		60
agcctctgct	tgtctgttct	cttgctgcga	tacagtctcg	gcgacggcag	ctgcagccga		120
cgatactgcg	acttgacggg	cgtcgggcga	atgtacttcg	tgctgcgatt	cacggacctg		180
ccgctcccg	agacgtgtcg	gtctcttgagc					210

```
<210> 20
<211> 70
<212> PRT
<213> Artificial
```

```
<220>
<221> misc_feature
<223> Description of Artificial Sequence: Sperm cell specific epitope M
      SA-6
```

```

<400>      20
Gln Pro Ser Glu Ala Ser Ser Gly Glu Val Ser Gly Asp Glu Ala Gly
1              5              10              15
Glu Gln Val Ser Ser Glu Thr Asn Asp Lys Glu Asn Asp Ala Met Ser
                20                25                30
Thr Pro Leu Pro Ser Thr Ser Ala Ala Ile Thr Leu Asn Cys His Thr
            35            40            45
Cys Ala Tyr Met Asn Asp Asp Ala Lys Cys Leu Arg Gly Glu Gly Val
        50          55          60
Cys Thr Thr Gln Asn Ser
65          70

```

<210>	21
<211>	45
<212>	DNA
<213>	Artificial

```
<220>
<221> misc_feature
<223> Description of Artificial Sequence: Oligomer from MSA 63
```

```
<400> 21
gtcggcagcc tccgaagcag cccgctccag agccccgtgc tccga 45
```

```
<210> 22
<211> 45
<212> DNA
<213> Artificial
```

```
<220>
<221> misc_feature
<223> Description of Artificial Sequence: Oligomer from MSA 63
```

```
<400> 22
agccccgtgc tccgaccgct cgtccagagc agcctctgct tgctg 45
```

```
<210> 23
<211> 45
<212> DNA
<213> Artificial
```

```

<220>
<221> misc_feature
<223> Description of Artificial Sequence: Oligomer from MSA 63

<400> 23
agcctctgct tgctgttcct cttgctgcga tacagctgcg gcgac 45

<210> 24
<211> 45
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description of Artificial Sequence: Oligomer from MSA 63

<400> 24
tacagctgcg gcgacggcag ctgcagccga cgatactgcg acttg 45

<210> 25
<211> 45
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description of Artificial Sequence: Oligomer from MSA 63

<400> 25
cgatactgcg acttgacggt gtgcacgcga atgtacttgc tgctg 45

<210> 26
<211> 45
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description of Artificial Sequence: Oligomer from MSA 63

<400> 26
atgtacttgc tgctgcgatt cacggacgcg ccgctcccg c agacg 45

<210> 27
<211> 45
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description of Artificial Sequence: Oligomer from MSA 63

<400> 27
cgattcacgg acgcgccgct cccgcagacg tgctgcgtct tgagc 45

<210> 28
<211> 17

```



```

<400> 31
gacattgtga tgtcacagtc tccatcctcc ctagctgtgt cagttggaga gaaggttact 60
atg 63

<210> 32
<211> 74
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description of Artificial Sequence: Consensus sequence

<400> 32
gcaagctcat agtaaccttc tctccaactg acacacgata gggaggatgg agactgtgac 60
atcacaaatgt ctgc 74

<210> 33
<211> 84
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Construct for MSA1 and MSALVAC-
1

<400> 33
agctgcgtcg gcagcctccg aagcagcccg ctccagagcc cgctgctggc atggtaccag 60
cagaaaccag ggcagtctcc taaa 84

<210> 34
<211> 72
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Construct for MSA1 and MSALVAC-
1

<400> 34
ctgccctggt ttctgctggt accatcggag cagcgggctc tgcgagcg gctgcttcgg 60
acggctgccg ac 72

<210> 35
<211> 78
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Construct for MSA1 and MSALVAC-
1

<400> 35

```

gacattgtga tgtcacagtc tccatcctcc ctagctgtgt cagttggaga gaaggttact 60  
gtgagcgcta agtccagt 78

<210> 36  
<211> 75  
<212> DNA  
<213> Artificial

<220>  
<221> misc\_feature  
<223> Description for Artificial Sequence: Construct for MSA1 and MSALVAC-  
1

<400> 36  
gagagccttt tatatagtag caatcaaaag atctacttgg cctggtacca gcagaaacca 60  
gggcagtctc ctaaa 75

<210> 37  
<211> 67  
<212> DNA  
<213> Artificial

<220>  
<221> misc\_feature  
<223> Description for Artificial Sequence: Construct for MSA1 and MSALVAC-  
1

<400> 37  
ctgctgattt actgggcatc cactagggaa tctgggggtcc ctgatcgctt cacaggctgg 60  
atctggg 67

<210> 38  
<211> 68  
<212> DNA  
<213> Artificial

<220>  
<221> misc\_feature  
<223> Description for Artificial Sequence: Construct for MSA1 and MSALVAC-  
1

<400> 38  
gcacagcaat attatagata tctcggacgt tcggtggagc caccaagctg caaatcaaac 60  
cggaattc 68

<210> 39  
<211> 69  
<212> DNA  
<213> Artificial

<220>  
<221> misc\_feature  
<223> Description for Artificial Sequence: Construct for MSA1 and MSALVAC-  
1

```

<400> 39
accgcctgtg aagcgatcag gcaccccaaga ttccctagtg gatgccagat aaatcagcag      60
tttaggaga                                     69

<210> 40
<211> 77
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Construct for MSA1 and MSALVAC-
1

<400> 40
ctgccctggt ttctgctggt accaggccaa gtagatcttt tgagattgct actatataaa      60
aggctctgac tggactt                                     77

<210> 41
<211> 78
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Construct for MSA1 and MSALVAC-
1

<400> 41
agcgctcata gtaaccttct ctccaactga cacagctagc gacgatcgag actgtgacat      60
cacaatgtct gcttgggc                                     78

<210> 42
<211> 78
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Construct for MSA1 and MSALVAC-
1

<400> 42
gaattcccgt ttgatttcca gcttgggtgcc tccaccgaac gtccgaggat atctataata      60
ttgctgtgcg taataaac                                     78

<210> 43
<211> 57
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Construct for MSA1 and MSALVAC-
1

```

<400> 43  
agagatttga gtctgaccat cagcagtgtg aaggctgaag acgtggcagt ttattac 57

<210> 44  
<211> 57  
<212> DNA  
<213> Artificial

<220>  
<221> misc\_feature  
<223> Description for Artificial Sequence: Construct for MSA1 and MSALVAC-1

<400> 44  
tgccaggtct tcagccttga cactgctgat ggtgagagtg aaatctgtcc cagatcc 57

<210> 45  
<211> 66  
<212> DNA  
<213> Artificial

<220>  
<221> misc\_feature  
<223> Description for Artificial Sequence: Construct for MSA1 and MSALVAC-1

<400> 45  
tcgtgccagt tctcgtcga ctagctcttc gactagctcc tgctgctctt gtcggtcacg 60  
gaattc 66

<210> 46  
<211> 75  
<212> DNA  
<213> Artificial

<220>  
<221> misc\_feature  
<223> Description for Artificial Sequence: Construct for MSA1 and MSALVAC-1

<400> 46  
gaattccgtg accgacaaga gcagcaggag ctagtcgaag agctggtcga cgaggaactg 60  
gcacgacggg ttcgt 75

<210> 47  
<211> 80  
<212> DNA  
<213> Artificial

<220>  
<221> misc\_feature  
<223> Description for Artificial Sequence: Constructs for LDH-C4

<400> 47  
gaattcatgg cttgggtgtg gaccttgcta ttctgatgg cagctgccca aagtgcccaa 60

```

gcacagatcc agttggtgca 80

<210> 48
<211> 79
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for LDH-C4

<400> 48
gtctggacct gagctgaaga agcctggaga gacagtcaag atctccgcta aggcttctgg 60
gtataccttc acaaactag 79

<210> 49
<211> 80
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVHCOL1

<400> 49
gaatgaactg ggtgaagcag gctccaggaa agggttttaa gtggatgggc tggataaaca 60
cctacactgg agagccaaca 80

<210> 50
<211> 80
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVHCOL1

<400> 50
tatgctgatg acttcaaggg acggtttgcc ttctctttgg aaacctctgc cagcactgcc 60
tatttgcaag atcaacacct 80

<210> 51
<211> 70
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVHCOL1

<400> 51
caaaaatgag gacacggcta catatttcgc tgcaagagcc tactatggta aatactttga 60
ctacgaattc 70

<210> 52
<211> 49
<212> DNA
<213> Artificial

```

```

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVHCOL1

<400> 52
gaattcgtag tcaaagtatt taccatagta ggctcttgca gcaaatatg 49

<210> 53
<211> 81
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVHCOL1

<400> 53
tagcctgtgt ctcatttttt gaggttggtg atctgcaaat aggcagtgtt ggcagagggt 60
tccaaagaga aggcaaaccg t 81

<210> 54
<211> 80
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVHCOL1

<400> 54
cccttgaagt catcagcata tgttggtctt ccagtgtagg tgtttatcca gcccatccac 60
tttaaaccct ttctggagc 80

<210> 55
<211> 81
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVHCOL1

<400> 55
ctgcttcacc cagttcattc catagtttgt gaagggtatac ccagaagcct tagcggagat 60
cttgactgtc tctccaaggc t 81

<210> 56
<211> 100
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVHCOL1

<400> 56
tcttcagctc aggtccagac tgcaccaact ggatctgtgc ttgggcactt tcggcagctg 60
ccatcaggaa tagcaaggtc cacaccaag ccatgaattc 100

```

```

<210> 57
<211> 63
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVHCOL1

<400> 57
agtattgtga tgaccagac tcccaaattc ctgcttgtat cagcaggaga cagggttacc 60
ata 63

<210> 58
<211> 64
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVHCOL1

<400> 58
acctgcaagg ccagtcagag tgtgagtaat gatgtagctt ggtaccaaca gaaaaccagg 60
gcag 64

<210> 59
<211> 69
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVLCOL1

<400> 59
tctcctaaac tgctgatata ctatgcatcc aatcgctaca ctggagtccc tgatcgcttc 60
actggcagt 69

<210> 60
<211> 64
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVLCOL1

<400> 60
ggatatggga cggatttcac tttcaccatc agcactgtgc aaggctgaag acctggcagt 60
ttat 64

<210> 61
<211> 69
<212> DNA
<213> Artificial

<220>

```

```

<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVLCOL1

<400> 61
ttctgycagc aggattatag ctctccgctc accttcggtg ctgggaccaa gctggacctg 60
aaagaattc 69

<210> 62
<211> 78
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVLCOL1

<400> 62
gaattctttc agctccagct tggccccagc accgaacgtg agcggagagc tataatcctg 60
ctgacagaaa taaactgc 78

<210> 63
<211> 63
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVLCOL1

<400> 63
caggtcttca gcctgcacag tgctgatggt gaaagtga aa tccgtcccat atccactgcc 60
agt 63

<210> 64
<211> 69
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVLCOL1

<400> 64
gaagcgatca gggactccag tgtagcgatt ggatgcatag tatatcagca gtttaggaga 60
ctgccctgg 69

<210> 65
<211> 63
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVLCOL1

<400> 65
tttctgttgg taccaagcta catcattact cacactctga ctggccttgc tggttatggt 60
aac 63

```

```

<210> 66
<211> 63
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVLCOL1

<400> 66
cctgtctcct gctcatacaa gcaggaattt gggagtctgg gtcatacaca tacttgcttg      60
ggc                                                                    63

<210> 67
<211> 68
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVLCOL1

<400> 67
ttcgctcagc aggattatag ctctccgctc acgttcggtg ctgggaccaa gctggagctg      60
aaagaatc                                                                    68

<210> 68
<211> 78
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVLCOL1

<400> 68
gaattctttc agctccagct tgggtcccagc accgaacgtg agcggagagc tataatcctg      60
ctgagcgaaa taaactgc                                                                    78

<210> 69
<211> 399
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Description for Artificial Sequence: Constructs for 2CAVLCOL1

<220>
<221> CDS
<222> (1)..(399)

<400> 69
atg gct tgg gtg tgg acc ttg cta ttc ctg atg gca gct gcc caa agt      48
Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
1          5          10          15

```

```

gcc caa gca gac att gtg atg tca cag tct cca tcc tcc cta gct gtg      96
Ala Gln Ala Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val
      20                      25                      30
tca gtt gga gag aag gtt act atg agc tgc aag tcc agt cag agc ctt      144
Ser Val Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu
      35                      40                      45
tta tat agt agc aat caa aag atc tac ttg gcc tgg tac cag cag aaa      192
Leu Tyr Ser Ser Asn Gln Lys Ile Tyr Leu Ala Trp Tyr Gln Gln Lys
      50                      55                      60
cca ggg cag tct cct aaa ctg ctg att tac tgg gca tcc act agg gaa      240
Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
      65                      70                      75                      80
tct ggg gtc cct gat cgc ttc aca ggc ggt gga tct ggg aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Thr Gly Gly Gly Ser Gly Thr Asp Phe
      85                      90                      95
act ctc acc atc agc agt gtg aag gct gaa gac ctg gca gtt tat tac      336
Thr Leu Thr Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr
      100                      105                      110
tgt cag caa tat tat aga tat cct cgg acg ttc ggt gga ggc acc aag      384
Cys Gln Gln Tyr Tyr Arg Tyr Pro Arg Thr Phe Gly Gly Gly Thr Lys
      115                      120                      125
ctg gaa atc aaa cgg
Leu Glu Ile Lys Arg
      130

```

<210> 70  
 <211> 133  
 <212> PRT  
 <213> Artificial

<220>  
 <221> misc\_feature  
 <223> Description for Artificial Sequence: Constructs for 2CAVLCOL1

```

<400> 70
Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
1                      5                      10                      15

Ala Gln Ala Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val
      20                      25                      30

Ser Val Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu
      35                      40                      45

Leu Tyr Ser Ser Asn Gln Lys Ile Tyr Leu Ala Trp Tyr Gln Gln Lys
      50                      55                      60

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
      65                      70                      75                      80

Ser Gly Val Pro Asp Arg Phe Thr Gly Gly Gly Ser Gly Thr Asp Phe
      85                      90                      95

Thr Leu Thr Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr
      100                      105                      110

Cys Gln Gln Tyr Tyr Arg Tyr Pro Arg Thr Phe Gly Gly Gly Thr Lys
      115                      120                      125

```

